

DNA: AGTAGTGTACTACCAAGTATAGATAACGTTTGAATATTAAGTTTTGAATC 51
 DNA: AAAGCCAAAGATGATTTGTATATTGGTGCTAATTACAGTTGCAGCTGCAAG 102
 M(1): M I C I L V L I T V A A A S

 DNA: CCCAGTGTATCAAAGGTGTTTCCAAGATGGGGCTATAGTGAAGCAAAACCC 153
 M(15): P V Y Q R C F Q D G A I V K Q N P

 DNA: ATCCAAAGAAGCAGTTACAGAGGTGTGCCTGAAAGATGATGTTAGCATGAT 204
 M(32): S K E A V T E V C L K D D V S M I

 DNA: CAAAACAGAGGCCAGGTATGTAAGAAATGCAACAGGAGTTTTTTTCAAATAA 255
 M(49): K T E A R Y V R N A T G V F S N N

 DNA: TGTGCAATAAGGAAATGGCTAGTCTCTGATTGGCATGATTGCAGGCCTAA 306
 M(66): V A I R K W L V S D W H D C R P K

 DNA: GAAGATCGTTGGGGGACACATCAATGTAATAGAAGTTGGTGATGACCTGTC 357
 M(83): K I V G G H I N V I E V G D D L S

 DNA: ACTCCATACTGAATCATATGTTTGCAGCGCAGATTGTACCATAGGTGTAGA 408
 M(100): L H T E S Y V C S A D C T I G V D

 DNA: CAAAGAGACTGCACAGGTCAGGCTTCAGACAGATACCACAAATCATTTTGA 459
 M(117): K E T A Q V R L Q T D T T N H F E

 DNA: AATTGCAGGCACTACTGTGAAGTCAGGATGGTTCAAGAGCACGACATATAT 510
 M(134): I A G T T V K S G W F K S T T Y I

 DNA: AACTCTTGATCAAACCTTGCGAACACCTTAAAGTTTCC TGCGGCCCAAAATC 561
 M(151): T L D Q T C E H L K V S C G P K S

 DNA: TGTACAGTTCCATGCCTGCTTCAATCAGCATATGTCTTGCGTCAGATTTTT 612
 M(168): V Q F H A C F N Q H M S C V R F L

 DNA: ACACAGGACAATATTGCCTGGCTCTATAGCCAATTCCATATGTCAGAATAT 663
 M(185): H R T I L P G S I A N S I C Q N I

 DNA: CGAAATCATAATTTTAGTTACACTTACTCTATTAATCTTTATATTGTTAAG 714
 M(202): E I I I L V T L T L L I F I L L S

 DNA: CATTTTAAGTAAGACTTATATATGTTATTTATTAATGCCTATATTCATCCC 765
 M(219): I L S K T Y I C Y L L M P I F I P

 DNA: CATAGCATATATATACGGTATAATTTACAATAAGTCGTGCAAAAAATGCAA 816
 M(236): I A Y I Y G I I Y N K S C K K C K

 DNA: ATTATGTGGCTTAGTGTATCATCCATTACAGAGTGTGGCACACATTGTGT 867
 M(253): L C G L V Y H P F T E C G T H C V

 DNA: CTGTGGTGCCCGCTATGATACTTCAGATAGAATGAACTGCATAGAGCTTC 918
 M(270): C G A R Y D T S D R M K L H R A S

 DNA: TGGATTGTGCCCTGGTTATAAAAGCCTAAGAGCTGCCAGAGTCATGTGCAA 969
 M(287): G L C P G Y K S L R A A R//V M C K

FIG. 1A

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DNA: GTCGAAAGGGCCTGCATCAATATTGTCTATAATTACTGCGGTACTGGTCTT 1020
M(304): S K G P A S I L S I I T A V L V L

DNA: AACCTTTGTGACACCAATCAACTCCATGGTTTTAGGAGAGAGTAAAGAAAC 1071
M(321): T F V T P I N S M V L G E S K E T

DNA: CTTTGAACCTGAAGATCTTCCAGACGACATGTTGGAAATGGCATCGAGAAT 1122
M(338): F E L E D L P D D M L E M A S R I

DNA: AAATTCTTATTATCTCACCTGTATCTTGAATTATGCTGTAAGCTGGGGTCT 1173
M(355): N S Y Y L T C I L N Y A V S W G L

DNA: TGTTATCATTGGATTGTTGATCGGGCTGCTTTTTAAGAAATACCAGCACAG 1224
M(372): V I I G L L I G L L F K K Y Q H R

DNA: ATTCTTAAATGTTTACGCAATGTACTGTGAAGAATGTGACATGTATCATGA 1275
M(389): F L N V Y A M Y C E E C D M Y H D

DNA: CAAGTCTGGGTTGAAAAGACATGGTGATTTTACCAACAAATGCAGACAGTG 1326
M(406): K S G L K R H G D F T N K C R Q C

DNA: CACATGTGGTCAATATGAAGATGCTGCAGGTTTGATGGCTCACAGGAAAAC 1377
M(423): T C G Q Y E D A A G L M A H R K T

DNA: CTATAACTGCTTAGTGCAGTACAAAGCAAAGTGGATGATGAACTTCCTGAT 1428
M(440): Y N C L V Q Y K A K W M M N F L I

DNA: AATTTACATATTCTTAATTTTGATCAAAGATTCTGCTATAGTTGTACAAGC 1479
M(457): I Y I F L I L I K D S A I V V Q A/

DNA: TGCTGGAACCTGACTTCACCACCTGCCTAGAGACTGAGAGTATAAATTGGAA 1530
M(474): /A G T D F T T C L E T E S I N W N

DNA: CTGCACTGGGCCATTTTTGAACCTCGGGAATTGCCAAAAGCAACAAAAGAA 1581
M(491): C T G P F L N L G N C Q K Q Q K K

DNA: AGAACCTTACACCAACATTGCAACTCAGTTAAAGGGACTAAAGGCAATTTT 1632
M(508): E P Y T N I A T Q L K G L K A I S

DNA: CGTACTAGATGTCCCTATAATAACAGGGATACCAGATGATATTGCGGGTGC 1683
M(525): V L D V P I I T G I P D D I A G A

DNA: TTTAAGATATATAGAAGAGAAGGAAGATTTCCATGTCCAGCTAACTATAGA 1734
M(542): L R Y I E E K E D F H V Q L T I E

DNA: ATATGCGATGTTAAGCAAATACTGTGACTATTATACCCAATTCTCAGATAA 1785
M(559): Y A M L S K Y C D Y Y T Q F S D N

DNA: CTCAGGATACAGTCAGACAACATGGAGAGTGTAAGGTCTCATGATTT 1836
M(576): S G Y S Q T T W R V Y L R S H D F

DNA: TGAAGCCTGTATACTATATCCAAATCAGCACTTTTGCAGATGTGTAAAAAA 1887
M(593): E A C I L Y P N Q H F C R C V K N

FIG. 1B

DNA: TGGTGAGAAAGTGCAGCAGCTCCAATTGGGACTTTGCCAATGAAATGAAAGA 1938
M(610): G E K C S S S N W D F A N E M K D

DNA: TTATTACTCTGGGAAACAAACAAAGTTTGACAAGGACTTAAA TCTAGCCCT 1989
M(627): Y Y S G K Q T K F D K D L N L A L

DNA: AACAGCTTTGCATCATGCCTTCAGGGGGACCTCATCTGCATA TATAGCAAC 2040
M(644): T A L H H A F R G T S S A Y I A T

DNA: AATGCTCTCAAAAAAGTCCAATGATGACTTGATTGCATACACAAATAAGAT 2091
M(661): M L S K K S N D D L I A Y T N K I

DNA: AAAAACAAAATTCCCAGGTAATGCATTGTTGAAGGCTATAATAGATTATAT 2142
M(678): K T K F P G N A L L K A I I D Y I

DNA: AGCATATATGAAAAGTTTGCCAGGTATGGCAAATTTCAAATATGATGAATT 2193
M(695): A Y M K S L P G M A N F K Y D E F

DNA: CTGGGATGAATTACTGTACAAACCCAAACCCAGCAAAGGCCTCAAACCTTGC 2244
M(712): W D E L L Y K P N P A K A S N L A

DNA: TAGAGGAAAGGAGTCATCTTACAACCTCAAACCTAGCAATTTCAATCAAAGTC 2295
M(729): R G K E S S Y N F K L A I S S K S

DNA: TATAAAAACCTGCAAGAATGTTAAGGATGTTGCCTGCTTATCGCCAAGGTC 2346
M(746): I K T C K N V K D V A C L S P R S

DNA: AGGTGCTATATATGCTTCAATAATTGCGTGTGGTGAACCCAAT GGGCCAAG 2397
M(763): G A I Y A S I I A C G E P N G P S

DNA: TGTGTATAGGAAACCATCAGGTGGTGTATTCCAATCTAGCACT GATCGGTC 2448
M(780): V Y R K P S G G V F Q S S T D R S

DNA: TATATACTGCTTGCTGGATAGCCATTGTCTAGAAGAATTTGAG GCCATCGG 2499
M(797): I Y C L L D S H C L E E F E A I G

DNA: CCAGGAGGAGCTGGATGCGGTAAAGAAATCCAAATGTTGGGAAATTGAATA 2550
M(814): Q E E L D A V K K S K C W E I E Y

DNA: TCCTGACGTAAAGCTCATCCAAGAAGGCGATGGGACTAAAAGCTGTAGAAT 2601
M(831): P D V K L I Q E G D G T K S C R M

DNA: GAAAGATTCTGGGAACTGCAATGTTGCAACTAACAGATGGCCAGTGATACA 2652
M(848): K D S G N C N V A T N R W P V I Q

DNA: ATGTGAGAATGACAAATTTTACTACTCAGAGCTTCAAAAAGATTATGACAA 2703
M(865): C E N D K F Y Y S E L Q K D Y D K

DNA: AGCTCAAGATATTGGTCACTATTGCTTAAGCCCTGGATGTACTACTGTCCG 2754
M(882): A Q D I G H Y C L S P G C T T V R

DNA: GTACCCTATTAATCCAAAGCATCTCTAACTGTAATTGGCAAGTAAGCAG 2805
M(899): Y P I N P K H I S N C N W Q V S R

FIG. 1C

DNA: ATCTAGCATAGCGAAGATAGATGTGCACAATATTGAGGATATTGAGCAATA 2856
M(916): S S I A K I D V H N I E D I E Q Y

DNA: TAAGAAAGCTATAACTCAGAAACTTCAAACGAGCCTATCTCTATTCAAGTA 2907
M(933): K K A I T Q K L Q T S L S L F K Y

DNA: TGCAAAAACAAAAAAGTTGCCGCACATCAAACCAATTTATAAATATATAAC 2958
M(950): A K T K N L P H I K P I Y K Y I T

DNA: TATAGAAGGAACAGAAACTGCAGAAGGTATAGAGAGTGCATACATTGAATC 3009
M(967): I E G T E T A E G I E S A Y I E S

DNA: AGAAGTACCTGCATTGGCTGGGACATCTATCGGATTCAAAATCAATTCTAA 3060
M(984): E V P A L A G T S I G F K I N S K

DNA: AGAGGGCAAGCACTTGCTAGATGTTATAGCATATGTAAAAAGTGCCTCATA 3111
M(1001): E G K H L L D V I A Y V K S A S Y

DNA: CTCTTCAGTGTATACAAAATTGTACTCAACTGGCCCAACATCAGGGATAAA 3162
M(1018): S S V Y T K L Y S T G P T S G I N

DNA: TACTAAACATGATGAATTGTGTACTGGCCCATGCCCAGCAAATATCAATCA 3213
M(1035): T K H D E L C T G P C P A N I N H

DNA: TCAGGTTGGGTGGCTGACATTTGCAAGAGAGAGGACAAGCTCATGGGGATG 3264
M(1052): Q V G W L T F A R E R T S S W G C

DNA: CGAAGAGTTTGGTTGCCTGGCTGTAAGTGATGGGTGTGTATTGGATCATG 3315
M(1069): E E F G C L A V S D G C V F G S C

DNA: CCAAGATATAATAAAAGAAGAACTATCTGTCTATAGGAAGGAGACCGAGGA 3366
M(1086): Q D I I K E E L S V Y R K E T E E

DNA: AGTGACTGATGTAGAACTGTGTTTGACATTTTCAGACAAAACATACTGTAC 3417
M(1103): V T D V E L C L T F S D K T Y C T

DNA: AAACTTAAACCCTGTTACCCCTATTATAACAGATCTATTTGAGGTACAGTT 3468
M(1120): N L N P V T P I I T D L F E V Q F

DNA: CAAAAGTGTAGAGACCTACAGCTTGCCTAGAATTGTTGCTGTGCAAAACCA 3519
M(1137): K T V E T Y S L P R I V A V Q N H

DNA: TGAGATTAAAATTGGGCAAATAAATGATTTAGGAGTTTACTCTAAGGGTTG 3570
M(1154): E I K I G Q I N D L G V Y S K G C

DNA: TGGGAATGTTCAAAGGTCAATGGAAGTATTTATGGCAATGGAGTTCCCAG 3621
M(1171): G N V Q K V N G T I Y G N G V P R

DNA: ATTTGACTACTTATGCCATTTAGCTAGCAGGAAGGAAGTCATTGTTAGAAA 3672
M(1188): F D Y L C H L A S R K E V I V R K

DNA: ATGCTTCGACAATGATTACCAAGCATGCAAATTTCTTCAAAGCCCTGCTAG 3723
M(1205): C F D N D Y Q A C K F L Q S P A S

FIG. 1D

DNA: TTACAGACTTGAAGAAGACAGTGGCACTGTGACCATAATTGACTACAAAAA 3774
M(1222): Y R L E E D S G T V T I I D Y K K

DNA: GATTTTAGGAACAATCAAGATGAAGGCAATTTTAGGAGATGTCAAATATAA 3825
M(1239): I L G T I K M K A I L G D V K Y K

DNA: AACATTTGCTGATAGTGTGATATAACCGCAGAAGGGTCATGCACCGGCTG 3876
M(1256): T F A D S V D I T A E G S C T G C

DNA: TATTAAGTCTTCGAAAATATCCATTGCGAATTAACGTTGCACACCACAAT 3927
M(1273): I N C F E N I H C E L T L H T T I

DNA: TGAAGCCAGCTGCCCAATTAAAAGCTCGTGCACAGTATTTTCATGACAGGAT 3978
M(1290): E A S C P I K S S C T V F H D R I

DNA: TCTTGTGACTCCAAATGAACACAAATATGCATTGAAAATGGTGTGCACAGA 4029
M(1307): L V T P N E H K Y A L K M V C T E

DNA: AAAGCCAGGGAACACACTCACAATTAAAGTCTGCAATACTAAAAGTTGAAGC 4080
M(1324): K P G N T L T I K V C N T K V E A

DNA: ATCTATGGCCCTTGTAAGACGCAAAGCCTATCATAGAAGTAGCACCAGTTGA 4131
M(1341): S M A L V D A K P I I E L A P V D

DNA: TCAGACAGCATATATAAGAGAAAAAGATGAAAGGTGTAAAGTTGGATGTG 4182
M(1358): Q T A Y I R E K D E R C K T W M C

DNA: TAGGGTAAGAGATGAAGGACTGCAGGTCTCTGGAGCCATTTAAAAATTT 4233
M(1375): R V R D E G L Q V I L E P F K N L

DNA: ATTTGGATCTTATATTGGGATATTTTACACATTTATTATATCTATAGTAGT 4284
M(1392): F G S Y I G I F Y T F I I S I V V

DNA: ATTATTGGTTATTATCTATGTACTACTACCTATATGCTTTAAGTTAAGGGA 4335
M(1409): L L V I I Y V L L P I C F K L R D

DNA: TACCCTTAGAAAGCATGAAGATGCATATAAGAGAGAGATGAAAATTAGATA 4386
M(1426): T L R K H E D A Y K R E M K I R ●

DNA: GGGGATCTATGCAGAACAAAATTGAGTCCTGTATTATATACTTCTATTTGT 4437
DNA: AGTATAGCTGTTGTTAAGTGGGGGTGGGGAACATAACAACAGCGTAAATTT 4488
DNA: ATTTTGCAACATTATTTTATACTTGGTAGCACACTACT 4527

FIG. 1E

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DNA: AGTAGTGTACCCCACTTGAATACTTTGAAAATAAATTGTTGTTGACTGTTT 51
 DNA: TTTACCTAAGGGGAAATTATCAAGAGTGTGATGTCGGATTGGTGTTTTAT 1 02
 N(1): M S D L V F Y
 NSs(1): M

DNA: GATGTCGCATCAACAGGTGCAAATGGATTGATCCTGATGCAGGGTATATG 1 53
 N(8): D V A S T G A N G F D P D A G Y M
 NSs(2): M S H Q Q V Q M D L I L M Q G I W

DNA: GACTTCTGTGTTAAAAATGCAGAATTACTCAACCTTGCTGCAGTTAGGATC 2 04
 N(25): D F C V K N A E L L N L A A V R I
 NSs(19): T S V L K M Q N Y S T L L Q L G S

DNA: TTCTTCCTCAATGCCGCAAAGGCCAAGGCTGCTCTCTCGCGTAAGCCAGAG 2 55
 N(42): F F L N A A K A K A A L S R K P E
 NSs(36): S S S M P Q R P R L L S R V S Q R

DNA: AGGAAGGCTAACCCTAAATTTGGAGAGTGGCAGGTGGAGGTTATCAATAAT 3 06
 N(59): R K A N P K F G E W Q V E V I N N
 NSs(53): G R L T L N L E S G R W R L S I I

DNA: CATTTTCCTGGAAACAGGAACAACCCAATTGGTAACAACGATCTTACCATC 3 57
 N(76): H F P G N R N N P I G N N D L T I
 NSs(70): I F L E T G T T Q L V T T I L P S

DNA: CACAGATTATCTGGGTATTTAGCCAGATGGGTCCTTGATCAGTATAACGAG 4 08
 N(93): H R L S G Y L A R W V L D Q Y N E
 NSs(87): T D Y L G I

DNA: AATGATGATGAGTCTCAGCACGAGTTGATCAGAACAACCTATTATCAACCCA 4 59
 N(110): N D D E S Q H E L I R T T I I N P

DNA: ATTGCTGAGTCTAATGGTGTAGGATGGGACAGTGGGCCAGAGATCTATCTA 5 10
 N(127): I A E S N G V G W D S G P E I Y L

DNA: TCATTCTTTCCAGGAACAGAAATGTTTTTGGAACTTTCAAATTCTACCCG 5 61
 N(144): S F F P G T E M F L E T F K F Y P

DNA: CTGACCATTGGAATTCACAGAGTCAAGCAAGGCATGATGGACCCTCAATAC 6 12
 N(161): L T I G I H R V K Q G M M D P Q Y

DNA: CTGAAGAAGGCCTTAAGGCAACGCTATGGCACTCTCACAGCAGATAAGTGG 6 63
 N(178): L K K A L R Q R Y G T L T A D K W

DNA: ATGTCACAGAAGGTTGCAGCAATTGCTAAGAGCCTGAAGGATGTAGAGCAG 7 14
 N(195): M S Q K V A A I A K S L K D V E Q

FIG. 2A

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| | |
|--|-----|
| DNA: CTTAAATGGGGAAAAGGAGGCCTGAGCGATACTGCTAAAACATTCCTGCAG | 765 |
| N(212): L K W G K G G L S D T A K T F L Q | |
| DNA: AAATTGGCATCAGGCTTCCATAAATATGGCATGAGGCATTCAAATTAGGT | 816 |
| N(229): K F G I R L P ● | |
| DNA: TCTAAATTCTAAATTTATATATGTCAATTTGATTAATTGGTTATCCAAAAG | 867 |
| DNA: GGTTTTCTTAAGGGAACCCACAAAAATAGCAGCTAAATGGGTGGGTGGTAG | 918 |
| DNA: GGGACAGCAAAAACTATAAATCAGGTCATAAATAAAATAAAATGTATTCA | 969 |
| DNA: GTGGGGCACACTACT | 984 |

FIG. 2B

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DNA: AGTAGTGTAACCCCTATCTACAAAACCTTACAGAAAATTTCAGTCATATCACAA 51
 DNA: TATATGCATAATGGACTATCAAGAGTATCAACAATTCTTGGCTAGGATTAA 102
 (L1): M D Y Q E Y Q Q F L A R I N

 DNA: TACTGCAAGGGATGCATGTGTAGCCAAGGATATCGATGTTGACCTATTAAT 153
 (L15): T A R D A C V A K D I D V D L L M

 DNA: GGCCAGACATGATTATTTTGGTAGAGAGCTGTGCAAGTCCTTAAATATAGA 204
 (L32): A R H D Y F G R E L C K S L N I E

 DNA: ATATAGGAATGATGTACCATTTGTAGATATAATTTTGGATATAAGGCCCGA 255
 (L49): Y R N D V P F V D I I L D I R P E

 DNA: AGTAGACCCATTAACCATAGATGCACCACATATTACCCCAGACAATTATCT 306
 (L66): V D P L T I D A P H I T P D N Y L

 DNA: ATATATAAATAATGTGTTATATATCATAGATTATAAGGTCTCTGTATCGAA 357
 (L83): Y I N N V L Y I I D Y K V S V S N

 DNA: TGAAAGCAGTGTATAACATATGACAAATATTATGAGTTAACTAGGGACAT 408
 (L100): E S S V I T Y D K Y Y E L T R D I

 DNA: ATCCGATAGATTAAGTATTCCAATAGAAATAGTTATCGTCCGTATAGACCC 459
 (L117): S D R L S I P I E I V I V R I D P

 DNA: TGTAAGTAAGGATTTGCATATTAACTCTGATAGATTTAAAGAACTTTACCC 510
 (L134): V S K D L H I N S D R F K E L Y P

 DNA: TACAATAGTGGTGGATATAAACTTCAATCAATTTTTCGACTTAAACAATT 561
 (L151): T I V V D I N F N Q F F D L K Q L

 DNA: ACTCTATGAAAAATTCGGTGATGATGAAGAATTCCTATTGAAAGTTGCACA 612
 (L168): L Y E K F G D D E E F L L K V A H

 DNA: TGGTGACTTCACTCTTACAGCACCCCTGGTGCAGACTGGGTGCCCTGAATT 663
 (L185): G D F T L T A P W C K T G C P E F

 DNA: TTGGAAACACCCCATTTATAAAGAATTTAAATGAGTATGCCAGTACCTGA 714
 (L202): W K H P I Y K E F K M S M P V P E

 DNA: GCGGAGGCTCTTTGAAGAATCTGTCAAGTTCAATGCTTATGAATCTGAGAG 765
 (L219): R R L F E E S V K F N A Y E S E R

 DNA: ATGGAATACTAACTTGGTTAAAAATCAGAGAATATACAAAGAAAGACTATTC 816
 (L236): W N T N L V K I R E Y T K K D Y S

 DNA: AGAGCATATTTCAAATCTGCAAAAAATATTTTCCTGGCTAGTGGATTTTA 867
 (L253): E H I S K S A K N I F L A S G F Y

 DNA: TAAGCAGCCAAATAAGAATGAGATTAGTGAGGGGTGGACATTAATGGTTGA 918
 (L270): K Q P N K N E I S E G W T L M V E

 DNA: GAGGGTTCAAGATCAGAGAGAAATCTCAAATCTCTCCATGACCAGAAACC 969
 (L287): R V Q D Q R E I S K S L H D Q K P

FIG. 3A

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DNA: TAGCATACATTTTATATGGGGAGCCCATAACCCAGGAAATAGTAATAATGC 1020
(L304): S I H F I W G A H N P G N S N N A

DNA: AACCTTCAAACCTCATATTGCTTTCAAAGTCCTTACAAAGCATAAAAGGTAT 1071
(L321): T F K L I L L S K S L Q S I K G I

DNA: ATCAACTTACACAGAAGCGTTCAAATCTTTAGGAAAAATGATGGATATTGG 1122
(L338): S T Y T E A F K S L G K M M D I G

DNA: AGATAAGGCTATTGAGTATGAAGAATTCTGCATGTCCCTAAAAAGCAAAGC 1173
(L355): D K A I E Y E E F C M S L K S K A

DNA: AAGATCATCATGGAAGCAAATAATGAACAAAAAATTAGAGCCTAAACAAAT 1224
(L372): R S S W K Q I M N K K L E P K Q I

DNA: AAACAATGCCCTTGTTTTATGGGAACAGCAGTTTATGGTAAATAATGACCT 1275
(L389): N N A L V L W E Q Q F M V N N D L

DNA: GATAGACAAAAGTGAGAAGTTGAAATTATTCAAAAATTTCTGCGGTATAGG 1326
(L406): I D K S E K L K L F K N F C G I G

DNA: CAAACACAAGCAATTCAAGAATAAAATGCTAGAGGATCTAGAAGTGTCAAA 1377
(L423): K H K Q F K N K M L E D L E V S K

DNA: GCCCAAAATATTAGACTTTGATGACGCAAATATGTATCTAGCTAGCCTAAC 1428
(L440): P K I L D F D D A N M Y L A S L T

DNA: CATGATGGAACAGAGTAAGAAGATATTGTCCAAAAGCAATGGGTGAAGCC 1479
(L457): M M E Q S K K I L S K S N G L K P

DNA: AGATAATTTTATACTGAATGAATTTGGATCCAAAATCAAAGATGCTAATAA 1530
(L474): D N F I L N E F G S K I K D A N K

DNA: AGAAACATATGACAATATGCACAAAATATTGAGACAAGATATTGGCAATG 1581
(L491): E T Y D N M H K I F E T R Y W Q C

DNA: TATATCCGACTTCTCTACTCTGATGAAAAATATCTTATCTGTGTCCCAATA 1632
(L508): I S D F S T L M K N I L S V S Q Y

DNA: TAACAGGCACAACACATTTAGGATAGCTATGTGTGCTAATAACAATGTCTT 1683
(L525): N R H N T F R I A M C A N N N V F

DNA: TGCTATAGTATTTTCTTCGGCTGACATAAAAACTAAGAAAGCAACTGTAGT 1734
(L542): A I V F P S A D I K T K K A T V V

DNA: TTATAGCATTATAGTGCTGCATAAAGAGGAAGAAAACATATTCAACCCAGG 1785
(L559): Y S I I V L H K E E E N I F N P G

DNA: ATGTTTGCACGGCACATTTAAGTGTATGAATGGGTATATTTCCATATCTAG 1836
(L576): C L H G T F K C M N G Y I S I S R

DNA: AGCTATAAGGCTAGATAAAGAGAGGTGCCAGAGAATTGTTTCCTCACCTGG 1887
(L593): A I R L D K E R C Q R I V S S P G

FIG. 3B

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| | |
|---|------|
| DNA: ACTGTTTTTAACAACCTTGCCTACTATTCAAACATGATAATCCAACCTCTAGT (L610): L F L T T C L L F K H D N P T L V | 1938 |
| DNA: GATGAGCGATATTATGAATTTTTCTATATACACTAGCCTGTCTATCACAAA (L627): M S D I M N F S I Y T S L S I T K | 1989 |
| DNA: GAGTGTTCCTATCTTTAACAGAGCCAGCAGCTACATGATTATGAACCTCATT (L644): S V L S L T E P A R Y M I M N S L | 2040 |
| DNA: AGCTATCTCCAGCAATGTTAAGGACTATATAGCAGAGAAATTTTCCCCTTA (L661): A I S S N V K D Y I A E K F S P Y | 2091 |
| DNA: CACAAAGACACTGTTCACTGTCTATATGACTAGACTAATTAAAAATGCTTG (L678): T K T L F S V Y M T R L I K N A C | 2142 |
| DNA: CTTTGATGCTTATGACCAGAGACAGCGTGTCCAACCTTAGAGATATATATTT (L695): F D A Y D Q R Q R V Q L R D I Y L | 2193 |
| DNA: ATCTGATTATGACATAACCCAAAAGGTATTAAAGACAATAGAGAGCTAAC (L712): S D Y D I T Q K G I K D N R E L T | 2244 |
| DNA: AAGTATATGGTTCCTGGTAGTGTAAACATTAAAGGAGTATTTAACACAAAT (L729): S I W F P G S V T L K E Y L T Q I | 2295 |
| DNA: ATACTTACCATTTTATTTTAAATGCTAAAGGACTACATGAGAAGCACCATGT (L746): Y L P F Y F N A K G L H E K H H V | 2346 |
| DNA: CATGGTGGATCTAGCAAAGACTATATTAGAAATAGAGTGCGAACAGAGGGA (L763): M V D L A K T I L E I E C E Q R E | 2397 |
| DNA: AAACATAAAGGAGATATGGTCTACAAATTGTACCAAACAGACAGTGAACCT (L780): N I K E I W S T N C T K Q T V N L | 2448 |
| DNA: TAAATTTTGTATCCATTCCTTGTGCAAGAATTTACTAGCAGACACTTCAAG (L797): K I L I H S L C K N L L A D T S R | 2499 |
| DNA: ACACAACCACTTGCGGAACAGAATAGAAAATAGGAACAATTTTAGAAGGTC (L814): H N H L R N R I E N R N N F R R S | 2550 |
| DNA: TATAACAACCTATTTCAACATTTACAAGTTCAAAGTCTTGCCTCAAAATAGG (L831): I T T I S T F T S S K S C L K I G | 2601 |
| DNA: GGACTTTAGAAAAGAGAAAGAGCTGCAGTCAGTTAAACAGAAGAAAATCTT (L848): D F R K E K E L Q S V K Q K K I L | 2652 |
| DNA: AGAGGTGCAGAGTCGCAAAATGAGATTAGCAAACCCAATGTTTCGTGACAGA (L865): E V Q S R K M R L A N P M F V T D | 2703 |
| DNA: TGAACAAGTATGCCTTGAAGTTGGGCACTGCAATTATGAGATGCTGAGGAA (L882): E Q V C L E V G H C N Y E M L R N | 2754 |
| DNA: TGCTATGCCGAATTATACAGATTATATATCAACTAAAGTATTTGATAGGTT (L899): A M P N Y T D Y I S T K V F D R L | 2805 |

FIG. 3C

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| | |
|---|------|
| DNA: ATATGAGTTATTAGATAAAGGAGTTTTGACAGACAAGCCTGTTATAGAGCA (L916): Y E L L D K G V L T D K P V I E Q | 2856 |
| DNA: AATAATGGATATGATGGTCGACCACAAAAAGTTCTATTTCACATTTTTCAA (L933): I M D M M V D H K K F Y F T F F N | 2907 |
| DNA: TAAAGGCCAGAAAACGTCAAAGGATAGAGAGATATTCGTTGGAGAATATGA (L950): K G Q K T S K D R E I F V G E Y E | 2958 |
| DNA: AGCTAAAATGTGTATGTACGCAGTTGAGAGAATAGCAAAAAGAAAGATGTAA (L967): A K M C M Y A V E R I A K E R C K | 3009 |
| DNA: ATTAAATCCTGATGAAATGATATCTGAGCCGGGTGATGGCAAGTTGAAGGT (L984): L N P D E M I S E P G D G K L K V | 3060 |
| DNA: GTTGGAGCAAAAATCAGAACAAGAAATTCGATTCTTGGTCGAGACTACAAG (L1001): L E Q K S E Q E I R F L V E T T R | 3111 |
| DNA: GCAAAAGAATCGTGAAATCGATGAGGCAATTGAAGCATTAGCTGCAGAAGG (L1018): Q K N R E I D E A I E A L A A E G | 3162 |
| DNA: ATATGAGAGTAATCTAGAAAAAATTGAAAAGCTTTCACCTGGCAAAGCAAA (L1035): Y E S N L E K I E K L S L G K A K | 3213 |
| DNA: GGGCCTAAAGATGGAAATAAATGCAGATATGTCTAAATGGAGTGCTCAGGA (L1052): G L K M E I N A D M S K W S A Q D | 3264 |
| DNA: TGTTTTTTATAAATATTTCTGGCTCATAGCCTTAGACCCTATCCTCTACCC (L1069): V F Y K Y F W L I A L D P I L Y P | 3315 |
| DNA: ACAGGAAAAAGAGAGAATATTATACTTTATGTGCAACTACATGGATAAAGA (L1086): Q E K E R I L Y F M C N Y M D K E | 3366 |
| DNA: ATTGATACTGCCAGATGAATTATTATTCAATTTGCTGGACCAAAAAGTTGC (L1103): L I L P D E L L F N L L D Q K V A | 3417 |
| DNA: ATACCAGAATGATATAATAGCTACTATGACTAATCAATTAAATTCAAATAC (L1120): Y Q N D I I A T M T N Q L N S N T | 3468 |
| DNA: AGTTCTGATAAAGAGAAATTGGCTCCAAGGGAATTTCAACTACACCTCAAG (L1137): V L I K R N W L Q G N F N Y T S S | 3519 |
| DNA: TTACGTCCATAGCTGCGCAATGTCTGTGTATAAAGAAATATTAAAAGAGGC (L1154): Y V H S C A M S V Y K E I L K E A | 3570 |
| DNA: CATAACATTACTAGACGGGTCTATATTAGTCAACTCATTAGTCCATTTCGGA (L1171): I T L L D G S I L V N S L V H S D | 3621 |
| DNA: TGATAACCAAACATCGATAACAATAGTTCAGGATAAGATGGAAAATGATAA (L1188): D N Q T S I T I V Q D K M E N D K | 3672 |
| DNA: AATTATAGATTTTGCAATGAAAAGATTTGAGAGAGCCTGTTTGACATTTGG (L1205): I I D F A M K E F E R A C L T F G | 3723 |

FIG. 3D

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DNA: ATGCCAAGCAAATATGAAAAAGACATATGTAACAAATTGCATAAAAGAGTT 3774
(L1222): C Q A N M K K T Y V T N C I K E F

DNA: TGTTTCATTATTTAACTTGTACGGCGAACCCTTTTCAATATATGGCAGATT 3825
(L1239): V S L F N L Y G E P F S I Y G R F

DNA: CCTATTAACATCTGTGGGTGATTGTGCCTATATAGGGCCTTATGAAGATTT 3876
(L1256): L L T S V G D C A Y I G P Y E D L

DNA: AGCTAGTCGAATATCATCAGCCCAGACAGCCATAAAGCATGGTTGTCCACC 3927
(L1273): A S R I S S A Q T A I K H G C P P

DNA: CAGTCTAGCATGGGTGTCCATAGCAATAAGTCATTGGATGACCTCTCTGAC 3978
(L1290): S L A W V S I A I S H W M T S L T

DNA: ATACAACATGCTACCAGGGCAGTCAAATGACCCAATTGATTATTTCCCTGC 4029
(L1307): Y N M L P G Q S N D P I D Y F P A

DNA: AGAAAAATAGGAAGGATATCCCTATAGAATTGAATGGTGTATTAGATGCTCC 4080
(L1324): E N R K D I P I E L N G V L D A P

DNA: ATTGTCAATGATTAGTACAGTTGGATTGGAATCTGGGAATTTATACTTCTT 4131
(L1341): L S M I S T V G L E S G N L Y F L

DNA: GATAAAGTTGTTGAGCAAATATACCCCGGTCATGCAGAAAAGAGAGTCAGT 4182
(L1358): I K L L S K Y T P V M Q K R E S V

DNA: AGTCAACCAAATAGCTGAAGTTAAGAACTGGAAGGTCGAGGATCTAACAGA 4233
(L1375): V N Q I A E V K N W K V E D L T D

DNA: CAATGAAATATTTAGACTTAAAATACTCAGATATTTAGTTCTAGATGCAGA 4284
(L1392): N E I F R L K I L R Y L V L D A E

DNA: GATGGACCCTAGTGATATTATGGGTGAGACAAGCGACATGAGAGGGAGGTC 4335
(L1409): M D P S D I M G E T S D M R G R S

DNA: TATTTTGACACCTAGAAAATTCACAACAGCAGGCAGTTTAAGGAAATTATA 4386
(L1426): I L T P R K F T T A G S L R K L Y

DNA: TTCTTTCAGTAAGTACCAGGATAGACTGTCTTCCCCTGGAGGCATGGTTGA 4437
(L1443): S F S K Y Q D R L S S P G G M V E

DNA: ATTGTTCACTTATTTGCTTGAGAAAACCTGAGTTGTTAGTGAATAAGGGGA 4488
(L1460): L F T Y L L E K P E L L V T K G E

DNA: AGATATGAAAGATTATATGGAATCTGTGATATTCCGATATAATTCCAAAAG 4539
(L1477): D M K D Y M E S V I F R Y N S K R

DNA: GTTCAAAGAAAGTTTGTCAATACAGAACCCAGCACAATTATTTATAGAACA 4590
(L1494): F K E S L S I Q N P A Q L F I E Q

DNA: GATATTGTTCTCACATAAGCCCATAATAGACTTTTCTGGTATCAGGGACAA 4641
(L1511): I L F S H K P I I D F S G I R D K

FIG. 3E

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DNA: ATATATAAACCTACATGATAGTAGAGCTCTAGAGAAGGAACCTGACATATT 4692
(L1528): Y I N L H D S R A L E K E P D I L

DNA: AGGAAAAGTAACATTTACAGAGGCTTATAGATTATTAATGAGGGACCTGTC 4743
(L1545): G K V T F T E A Y R L L M R D L S

DNA: TAGCCTAGAACTAACCAATGATGACATTCAAGTAATTTATTCTTACATAAT 4794
(L1562): S L E L T N D D I Q V I Y S Y I I

DNA: ACTTAATGACCCTATGATGATAACTATTGCAAACACACATATATTGTCAAT 4845
(L1579): L N D P M M I T I A N T H I L S I

DNA: ATACGGGAGTCCTCAACGGAGGATGGGCATGTCCTGTTCAACGATGCCAGA 4896
(L1596): Y G S P Q R R M G M S C S T M P E

DNA: ATTTAGAAAATTTAAAATTAATACATCATTCCCCAGCCTTAGTTTTGAGAGC 4947
(L1613): F R N L K L I H H S P A L V L R A

DNA: ATATAGTAAAAATAATCCTGACATCCAGGGTGCTGATCCACGGAAATGGC 4998
(L1630): Y S K N N P D I Q G A D P T E M A

DNA: TAGAGATTTAGTTCATCTGAAAGAGTTTGTTGAGAACACAAATTTAGAAGA 5049
(L1647): R D L V H L K E F V E N T N L E E

DNA: AAAAATGAAAGTTAGGATTGCTATAAATGAAGCAGAGAAAGGACAACGGGA 5100
(L1664): K M K V R I A I N E A E K G Q R D

DNA: TATAGTCTTTGAACTAAAAGAGATGACTAGATTTTATCAGGTTTGCTATGA 5151
(L1681): I V F E L K E M T R F Y Q V C Y E

DNA: GTATGTCAAATCTACAGAACACAAGATAAAAAGTCTTCATTCTCCCGACAAA 5202
(L1698): Y V K S T E H K I K V F I L P T K

DNA: ATCATACACAACAACAGATTTCTGTTCATCATGCAGGGGAATTTAATAAA 5253
(L1715): S Y T T T D F C S L M Q G N L I K

DNA: AGATAAAGAGTGGTACACAGTTCACTACCTAAAACAGATATTGTCTGGTGG 5304
(L1732): D K E W Y T V H Y L K Q I L S G G

DNA: CCATAAAGCCATAATGCAGCATAATGCCACTAGTGAGCAAAATATTGCTTT 5355
(L1749): H K A I M Q H N A T S E Q N I A F

DNA: TGAGTGTTTCAAATTAATTACCCATTTTGCAGACTCATTATAGATTTCATT 5406
(L1766): E C F K L I T H F A D S F I D S L

DNA: ATCTAGGTCAGCTTTTTTGCAGTTGATAATAGATGAATTCAGTTATAAAGA 5457
(L1783): S R S A F L Q L I I D E F S Y K D

DNA: TGTGAAGGTTAGCAAACTTTATGACATAATAAAGAATGGGTATAATCGAAC 5508
(L1800): V K V S K L Y D I I K N G Y N R T

DNA: TGACTTCATACCATTTGCTTTTTAGAACTGGCGATTTAAGACAAGCTGACTT 5559
(L1817): D F I P L L F R T G D L R Q A D L

FIG. 3F

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DNA: AGACAAGTATGATGCTATGAAAAGTCATGAGAGGGTTACATGGAATGATTG 5610
(L1834): D K Y D A M K S H E R V T W N D W

DNA: GCAAACATCTCGTCACTTGGACATGGGCTCAATTAATCTAACAATAACCGG 5661
(L1851): Q T S R H L D M G S I N L T I T G

DNA: TTACAATAGATCAATAACAATAATCGGAGAAGATAACAAATTGACATATGC 5712
(L1868): Y N R S I T I I G E D N K L T Y A

DNA: AGAATTATGTCTGACTAGGAAAACCTCTGAGAATATAACTATAAGTGGCAG 5763
(L1885): E L C L T R K T P E N I T I S G R

DNA: AAAATTGCTAGGTGCAAGGCATGGACTTAAATTTGAAAATATGTCCAAAAT 5814
(L1902): K L L G A R H G L K F E N M S K I

DNA: CCAAACATACCCAGGCAATTATTATATAACATATAGAAAGAAAGATCGCCA 5865
(L1919): Q T Y P G N Y Y I T Y R K K D R H

DNA: CCAGTTTGTATACCAGATACATTCTCATGAATCAATAACAAGGAGGAATGA 5916
(L1936): Q F V Y Q I H S H E S I T R R N E

DNA: AGAGCATATGGCTATCAGGACCAGAATATACAATGAAATAACTCCAGTATG 5967
(L1953): E H M A I R T R I Y N E I T P V C

DNA: TGTAGTTAACGTTGCAGAGGTGGATGGGGACCAACGTATATTGATAAGATC 6018
(L1970): V V N V A E V D G D Q R I L I R S

DNA: TTTAGACTATCTAAATAATGATATATTTTCTCTTTCAAGGATTAAAGTCGG 6069
(L1987): L D Y L N N D I F S L S R I K V G

DNA: GCTTGACGAATTTGCAACAATAAAAAAAGCACACTTTAGTAAATGGTCTC 6120
(L2004): L D E F A T I K K A H F S K M V S

DNA: ATTTGAAGGACCCCAATTAAGACAGGGCTCCTCGACCTTACTGAATTGAT 6171
(L2021): F E G P P I K T G L L D L T E L M

DNA: GAAATCTCAAGATTTGCTTAACCTTAATTATGATAATATAAGGAATAGCAA 6222
(L2038): K S Q D L L N L N Y D N I R N S N

DNA: CTTGATATCTTTTTCAAAATTGATTGCTGTGAGGGGTCAGATAATATAAA 6273
(L2055): L I S F S K L I C C E G S D N I N

DNA: TGATGGGTTAGAGTTTCTGTCCGATGACCCTATGAACCTTTACAGAGGGTGA 6324
(L2072): D G L E F L S D D P M N F T E G E

DNA: AGCAATACATTCAACACCGATCTTTAATATATATTACTCAAAAAGAGGAGA 6375
(L2089): A I H S T P I F N I Y Y S K R G E

DNA: AAGACATATGACATACAGGAATGCAATTAAATTACTGATAGAAAGAGAAAC 6426
(L2106): R H M T Y R N A I K L L I E R E T

DNA: TAAGATTTTGAAGAAGCTTTCACATTCAAGTGAAGATGGCTTCATATCGCC 6477
(L2123): K I F E E A F T F S E N G F I S P

FIG. 3G

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FIG. 3H

6528 DNA: AGAATCTTGGTTCCTTGAAGCAGTAGTATTAATAAATTGTTGAA
 (L2140): E N L G C L E A V V S L I K L K
 6579 DNA: AACTAATGAGTGGTCCACAGTTATAGATTAATAATGATATATGTTAAT
 (L2157): T N E W S T V I D K C I H I C L I
 6630 DNA: AAAGAATGGTATGGATCCACATGTTACCATTCATTTGATGTCCTTAATAATGTTT
 (L2174): K N G M D H M Y H S F D V P K C F
 6681 DNA: TATGGGAATCCTATCAGTATGAGATGATGATGTTTGAAGAAATT
 (L2191): M G N P I T R D M N W M M F R E F
 6732 DNA: CATCAATAGTTTACCGGAGCAGATATACCAATGGAATGTCATGACAGA
 (L2208): I N S L P G T D I P W N V M T E
 6783 DNA: GAACCTCAAAAAGAAAATGTAATTGCTCTGATTAACCTTAAGTTAGAAAACACA
 (L2225): N F K K K C I A L I N S K L E T Q
 6834 DNA: GAGAGATTTCTCAGAAATTCACCTAAACTGATGAATAAAGGAGGCTGGAGGAG
 (L2242): R D F S E F T K L M K K E G G R S
 6885 DNA: TAATATAGAATTTTGATTTAGTATGATTTTACAGAGAACCCTACAAATTAG
 (L2259): N I E F D ●
 6936 DNA: GCTATAAATTTGGGAGGGTTTGGAAATTTGGCTAATAAATTCAAAAAGAGGGG
 6980 DNA: GATTAAACAGCAACTGTATTAATTTTGATAGATGAGGGGCCACACTACT



A primer = cDNA primer = sense primer = forward primer =

B primer = antisense primer=reverse primer =

V = viral genome, minus (-) strand = —————

cV = viral antigenomic, plus strand (+) = —

cdNA or cRNA = complementary DNA or RNA = - - - - -

FIG. 4A

P1 = probe (sense or antisense) or capture oligo (sense or antisense)

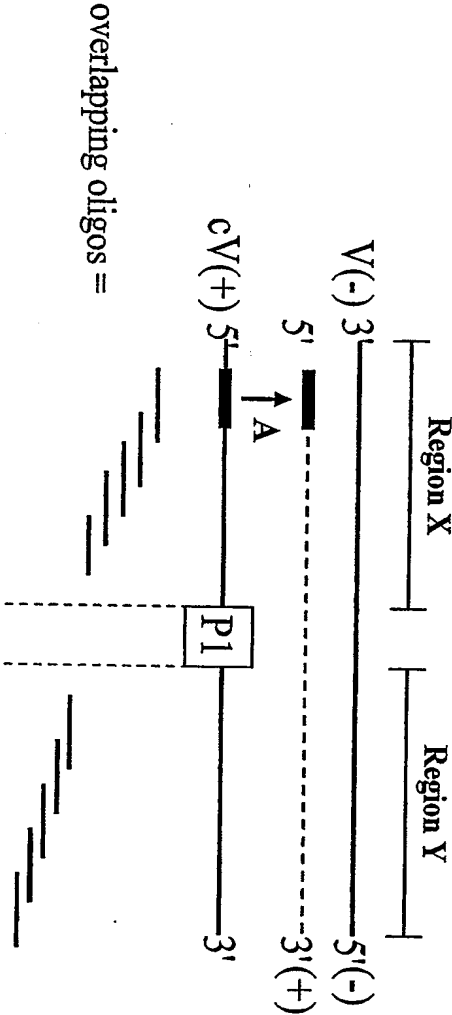


FIG. 4B

P1 = sense, cDNA primer (A)

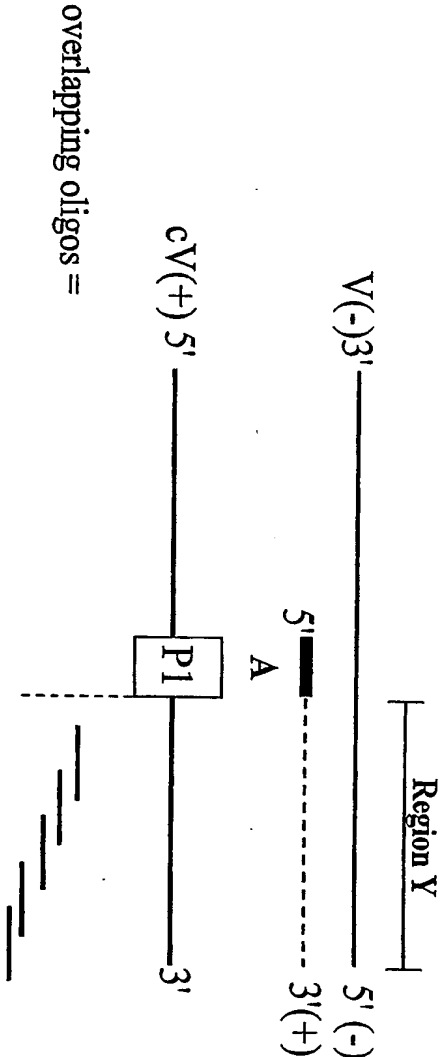


FIG. 4C

P1 = reverse, antisense primer (B)

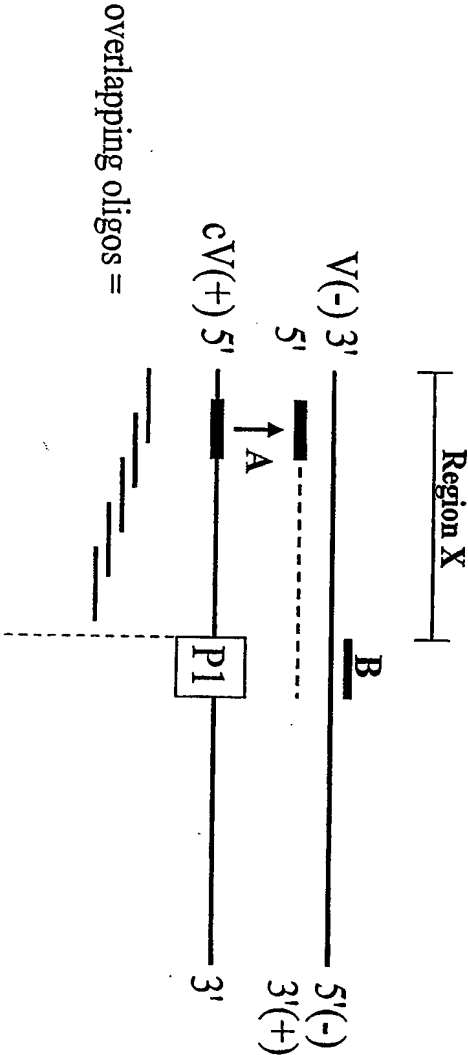


FIG. 4D

P1 = sense, cDNA primer and P2 = reverse, antisense primer

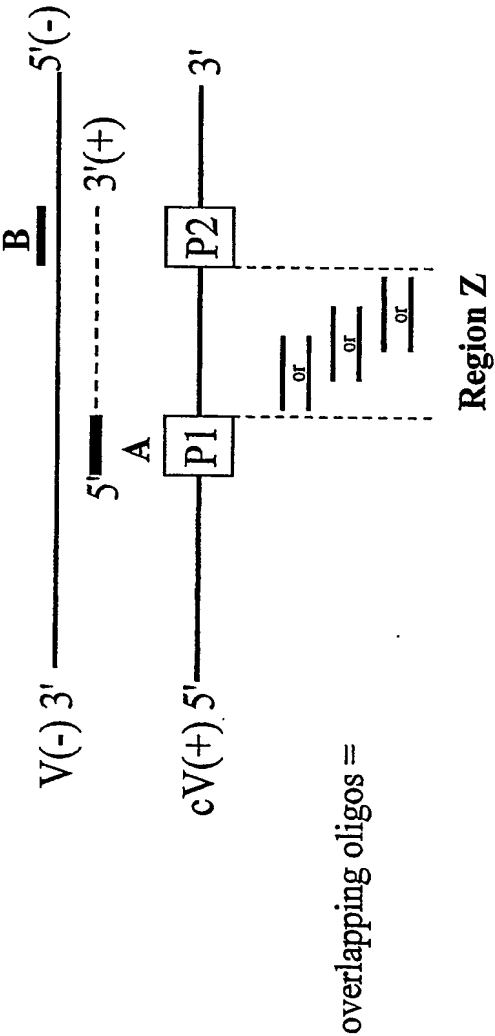


FIG. 4E

P1 = sense, cDNA primer and P2 = probe (sense or antisense)

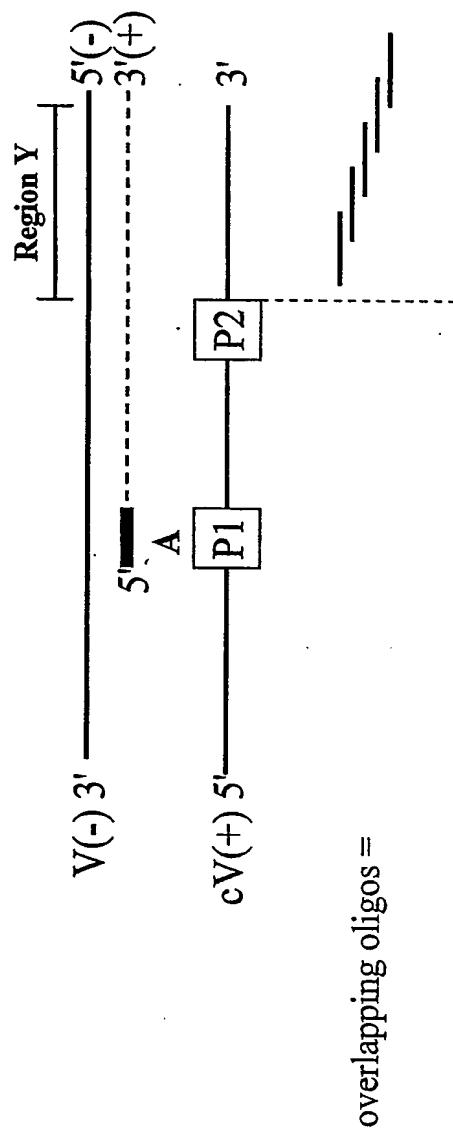


FIG. 4F

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FIG. 5A

Forward Primer

| Start | Length | Tm | %GC | Primer |
|-------|--------|----|-----|---------------------------|
| 1470 | 25 | 60 | 44 | TTGTACAAGCTGCTGGAAGTGAAGT |
| 1470 | 25 | 60 | 44 | TTGTACAAGCTGCTGGAAGTGAAGT |
| 1470 | 25 | 60 | 44 | TTGTACAAGCTGCTGGAAGTGAAGT |
| 1470 | 25 | 60 | 44 | TTGTACAAGCTGCTGGAAGTGAAGT |
| 1470 | 25 | 60 | 44 | TTGTACAAGCTGCTGGAAGTGAAGT |
| 1470 | 25 | 60 | 44 | TTGTACAAGCTGCTGGAAGTGAAGT |
| 1470 | 25 | 60 | 44 | TTGTACAAGCTGCTGGAAGTGAAGT |
| 1470 | 25 | 60 | 44 | TTGTACAAGCTGCTGGAAGTGAAGT |
| 1470 | 25 | 60 | 44 | TTGTACAAGCTGCTGGAAGTGAAGT |
| 1470 | 25 | 60 | 44 | TTGTACAAGCTGCTGGAAGTGAAGT |
| 1470 | 25 | 60 | 44 | TTGTACAAGCTGCTGGAAGTGAAGT |
| 1470 | 25 | 60 | 44 | TTGTACAAGCTGCTGGAAGTGAAGT |
| 869 | 22 | 60 | 50 | TGTGGTGCCCGCTATGATACTT |
| 869 | 22 | 60 | 50 | TGTGGTGCCCGCTATGATACTT |
| 869 | 22 | 60 | 50 | TGTGGTGCCCGCTATGATACTT |
| 869 | 22 | 60 | 50 | TGTGGTGCCCGCTATGATACTT |
| 869 | 22 | 60 | 50 | TGTGGTGCCCGCTATGATACTT |
| 869 | 20 | 58 | 55 | TGTGGTGCCCGCTATGATAC |
| 869 | 20 | 58 | 55 | TGTGGTGCCCGCTATGATAC |
| 869 | 20 | 58 | 55 | TGTGGTGCCCGCTATGATAC |
| 869 | 20 | 58 | 55 | TGTGGTGCCCGCTATGATAC |
| 869 | 20 | 58 | 55 | TGTGGTGCCCGCTATGATAC |
| 868 | 21 | 59 | 57 | CTGTGGTGCCCGCTATGATAC |
| 868 | 21 | 59 | 57 | CTGTGGTGCCCGCTATGATAC |
| 868 | 21 | 59 | 57 | CTGTGGTGCCCGCTATGATAC |
| 868 | 21 | 59 | 57 | CTGTGGTGCCCGCTATGATAC |
| 868 | 21 | 59 | 57 | CTGTGGTGCCCGCTATGATAC |
| 868 | 20 | 58 | 55 | CTGTGGTGCCCGCTATGATA |
| 868 | 20 | 58 | 55 | CTGTGGTGCCCGCTATGATA |
| 868 | 20 | 58 | 55 | CTGTGGTGCCCGCTATGATA |
| 868 | 20 | 58 | 55 | CTGTGGTGCCCGCTATGATA |
| 868 | 20 | 58 | 55 | CTGTGGTGCCCGCTATGATA |
| 867 | 21 | 60 | 52 | TCTGTGGTGCCCGCTATGATA |
| 867 | 21 | 60 | 52 | TCTGTGGTGCCCGCTATGATA |
| 867 | 21 | 60 | 52 | TCTGTGGTGCCCGCTATGATA |
| 867 | 21 | 60 | 52 | TCTGTGGTGCCCGCTATGATA |
| 867 | 20 | 60 | 55 | TCTGTGGTGCCCGCTATGAT |
| 867 | 20 | 60 | 55 | TCTGTGGTGCCCGCTATGAT |
| 867 | 20 | 60 | 55 | TCTGTGGTGCCCGCTATGAT |
| 867 | 20 | 60 | 55 | TCTGTGGTGCCCGCTATGAT |
| 867 | 20 | 60 | 55 | TCTGTGGTGCCCGCTATGAT |
| 864 | 20 | 60 | 60 | GTGTCTGTGGTGCCCGCTAT |
| 864 | 20 | 60 | 60 | GTGTCTGTGGTGCCCGCTAT |
| 864 | 20 | 60 | 60 | GTGTCTGTGGTGCCCGCTAT |

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FIG. 5B

| Forward Primer | | | | |
|----------------|--------|----|-----|---------------------------|
| Start | Length | Tm | %GC | Primer |
| 864 | 20 | 60 | 60 | GTGTCTGTGGTGCCCGCTAT |
| 864 | 20 | 60 | 60 | GTGTCTGTGGTGCCCGCTAT |
| 3739 | 23 | 68 | 48 | AGACAGTGGCACTGTGACCATAA |
| 3739 | 23 | 68 | 48 | AGACAGTGGCACTGTGACCATAA |
| 3739 | 23 | 68 | 48 | AGACAGTGGCACTGTGACCATAA |
| 3739 | 23 | 68 | 48 | AGACAGTGGCACTGTGACCATAA |
| 3739 | 23 | 68 | 48 | AGACAGTGGCACTGTGACCATAA |
| 3739 | 23 | 68 | 48 | AGACAGTGGCACTGTGACCATAA |
| 3739 | 23 | 68 | 48 | AGACAGTGGCACTGTGACCATAA |
| 3739 | 23 | 68 | 48 | AGACAGTGGCACTGTGACCATAA |
| 3739 | 24 | 69 | 46 | AGACAGTGGCACTGTGACCATAAT |
| 3739 | 24 | 69 | 46 | AGACAGTGGCACTGTGACCATAAT |
| 3739 | 24 | 69 | 46 | AGACAGTGGCACTGTGACCATAAT |
| 3739 | 24 | 69 | 46 | AGACAGTGGCACTGTGACCATAAT |
| 3739 | 24 | 69 | 46 | AGACAGTGGCACTGTGACCATAAT |
| 3739 | 24 | 69 | 46 | AGACAGTGGCACTGTGACCATAAT |
| 3739 | 24 | 69 | 46 | AGACAGTGGCACTGTGACCATAAT |
| 3738 | 23 | 68 | 48 | AAGACAGTGGCACTGTGACCATA |
| 3738 | 23 | 68 | 48 | AAGACAGTGGCACTGTGACCATA |
| 3738 | 23 | 68 | 48 | AAGACAGTGGCACTGTGACCATA |
| 3738 | 23 | 68 | 48 | AAGACAGTGGCACTGTGACCATA |
| 3738 | 23 | 68 | 48 | AAGACAGTGGCACTGTGACCATA |
| 3738 | 23 | 68 | 48 | AAGACAGTGGCACTGTGACCATA |
| 3738 | 23 | 68 | 48 | AAGACAGTGGCACTGTGACCATA |
| 3738 | 24 | 60 | 46 | AAGACAGTGGCACTGTGACCATAA |
| 3738 | 24 | 60 | 46 | AAGACAGTGGCACTGTGACCATAA |
| 3738 | 24 | 60 | 46 | AAGACAGTGGCACTGTGACCATAA |
| 3738 | 24 | 60 | 46 | AAGACAGTGGCACTGTGACCATAA |
| 3738 | 24 | 60 | 46 | AAGACAGTGGCACTGTGACCATAA |
| 3738 | 24 | 60 | 46 | AAGACAGTGGCACTGTGACCATAA |
| 3738 | 24 | 60 | 46 | AAGACAGTGGCACTGTGACCATAA |
| 3738 | 25 | 60 | 44 | AAGACAGTGGCACTGTGACCATAAT |
| 3738 | 25 | 60 | 44 | AAGACAGTGGCACTGTGACCATAAT |
| 3738 | 25 | 60 | 44 | AAGACAGTGGCACTGTGACCATAAT |
| 3738 | 25 | 60 | 44 | AAGACAGTGGCACTGTGACCATAAT |
| 3738 | 25 | 60 | 44 | AAGACAGTGGCACTGTGACCATAAT |
| 3738 | 25 | 60 | 44 | AAGACAGTGGCACTGTGACCATAAT |
| 3737 | 24 | 60 | 50 | GAAGACAGTGGCACTGTGACCATA |
| 3737 | 24 | 60 | 50 | GAAGACAGTGGCACTGTGACCATA |
| 3737 | 24 | 60 | 50 | GAAGACAGTGGCACTGTGACCATA |
| 3737 | 24 | 60 | 50 | GAAGACAGTGGCACTGTGACCATA |
| 3737 | 24 | 60 | 50 | GAAGACAGTGGCACTGTGACCATA |
| 3737 | 24 | 60 | 50 | GAAGACAGTGGCACTGTGACCATA |
| 3738 | 25 | 61 | 48 | AGAAGACAGTGGCACTGTGACCATA |

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FIG. 5C

| Forward Primer | | | | |
|----------------|--------|----|-----|---------------------------|
| Start | Length | Tm | %GC | Primer |
| 3738 | 25 | 61 | 48 | AGAAGACAGTGGCACTGTGACCATA |
| 3738 | 25 | 61 | 48 | AGAAGACAGTGGCACTGTGACCATA |
| 3738 | 25 | 61 | 48 | AGAAGACAGTGGCACTGTGACCATA |
| 3738 | 25 | 61 | 48 | AGAAGACAGTGGCACTGTGACCATA |
| 3738 | 25 | 61 | 48 | AGAAGACAGTGGCACTGTGACCATA |
| 3738 | 25 | 61 | 48 | AGAAGACAGTGGCACTGTGACCATA |
| 3739 | 23 | 58 | 48 | AGACAGTGGCACTGTGACCATAA |
| 3739 | 23 | 58 | 48 | AGACAGTGGCACTGTGACCATAA |
| 3739 | 23 | 58 | 48 | AGACAGTGGCACTGTGACCATAA |
| 3739 | 23 | 58 | 48 | AGACAGTGGCACTGTGACCATAA |
| 3739 | 23 | 58 | 48 | AGACAGTGGCACTGTGACCATAA |
| 3739 | 23 | 58 | 48 | AGACAGTGGCACTGTGACCATAA |
| 3739 | 24 | 59 | 46 | AGACAGTGGCACTGTGACCATAAT |
| 3739 | 24 | 59 | 46 | AGACAGTGGCACTGTGACCATAAT |
| 3739 | 24 | 59 | 46 | AGACAGTGGCACTGTGACCATAAT |
| 3739 | 24 | 59 | 46 | AGACAGTGGCACTGTGACCATAAT |
| 3739 | 24 | 59 | 46 | AGACAGTGGCACTGTGACCATAAT |
| 3739 | 24 | 59 | 46 | AGACAGTGGCACTGTGACCATAAT |
| 3739 | 24 | 59 | 46 | AGACAGTGGCACTGTGACCATAAT |
| 3738 | 23 | 58 | 48 | AAGACAGTGGCACTGTGACCATA |
| 3738 | 23 | 58 | 48 | AAGACAGTGGCACTGTGACCATA |
| 3738 | 23 | 58 | 48 | AAGACAGTGGCACTGTGACCATA |
| 3738 | 23 | 58 | 48 | AAGACAGTGGCACTGTGACCATA |
| 3738 | 23 | 58 | 48 | AAGACAGTGGCACTGTGACCATA |
| 3738 | 23 | 58 | 48 | AAGACAGTGGCACTGTGACCATA |
| 3738 | 24 | 60 | 46 | AAGACAGTGGCACTGTGACCATAA |
| 3738 | 24 | 60 | 46 | AAGACAGTGGCACTGTGACCATAA |
| 3738 | 24 | 60 | 46 | AAGACAGTGGCACTGTGACCATAA |
| 3738 | 24 | 60 | 46 | AAGACAGTGGCACTGTGACCATAA |
| 3738 | 24 | 60 | 46 | AAGACAGTGGCACTGTGACCATAA |
| 3738 | 24 | 60 | 46 | AAGACAGTGGCACTGTGACCATAA |
| 3738 | 25 | 60 | 44 | AAGACAGTGGCACTGTGACCATAAT |
| 3738 | 25 | 60 | 44 | AAGACAGTGGCACTGTGACCATAAT |
| 3738 | 25 | 60 | 44 | AAGACAGTGGCACTGTGACCATAAT |
| 3738 | 25 | 60 | 44 | AAGACAGTGGCACTGTGACCATAAT |
| 3738 | 25 | 60 | 44 | AAGACAGTGGCACTGTGACCATAAT |
| 3738 | 25 | 60 | 44 | AAGACAGTGGCACTGTGACCATAAT |
| 3737 | 24 | 60 | 50 | GAAGACAGTGGCACTGTGACCATA |
| 3737 | 24 | 60 | 50 | GAAGACAGTGGCACTGTGACCATA |
| 3737 | 24 | 60 | 50 | GAAGACAGTGGCACTGTGACCATA |
| 3737 | 24 | 60 | 50 | GAAGACAGTGGCACTGTGACCATA |

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FIG. 5D

| Forward Primer | | | | |
|----------------|--------|----|-----|---------------------------|
| Start | Length | Tm | %GC | Primer |
| 3737 | 24 | 60 | 50 | GAAGACAGTGGCACTGTGACCATA |
| 3737 | 24 | 60 | 50 | GAAGACAGTGGCACTGTGACCATA |
| 3737 | 24 | 60 | 50 | GAAGACAGTGGCACTGTGACCATA |
| 3738 | 25 | 61 | 48 | AGAAGACAGTGGCACTGTGACCATA |
| 3738 | 25 | 61 | 48 | AGAAGACAGTGGCACTGTGACCATA |
| 3738 | 25 | 61 | 48 | AGAAGACAGTGGCACTGTGACCATA |
| 3738 | 25 | 61 | 48 | AGAAGACAGTGGCACTGTGACCATA |
| 3738 | 25 | 61 | 48 | AGAAGACAGTGGCACTGTGACCATA |
| 3738 | 25 | 61 | 48 | AGAAGACAGTGGCACTGTGACCATA |
| 3738 | 25 | 61 | 48 | AGAAGACAGTGGCACTGTGACCATA |
| 3738 | 25 | 61 | 48 | AGAAGACAGTGGCACTGTGACCATA |
| 3739 | 23 | 58 | 48 | AGACAGTGGCACTGTGACCATAA |
| 3739 | 23 | 58 | 48 | AGACAGTGGCACTGTGACCATAA |
| 3739 | 23 | 58 | 48 | AGACAGTGGCACTGTGACCATAA |
| 3739 | 23 | 58 | 48 | AGACAGTGGCACTGTGACCATAA |
| 3739 | 23 | 58 | 48 | AGACAGTGGCACTGTGACCATAA |
| 3739 | 23 | 58 | 48 | AGACAGTGGCACTGTGACCATAA |
| 3739 | 23 | 58 | 48 | AGACAGTGGCACTGTGACCATAA |
| 3739 | 24 | 59 | 46 | AGACAGTGGCACTGTGACCATAAT |
| 3739 | 24 | 59 | 46 | AGACAGTGGCACTGTGACCATAAT |
| 3739 | 24 | 59 | 46 | AGACAGTGGCACTGTGACCATAAT |
| 3739 | 24 | 59 | 46 | AGACAGTGGCACTGTGACCATAAT |
| 3739 | 24 | 59 | 46 | AGACAGTGGCACTGTGACCATAAT |
| 3739 | 23 | 58 | 48 | AGACAGTGGCACTGTGACCATAA |
| 3739 | 23 | 58 | 48 | AGACAGTGGCACTGTGACCATAA |
| 3739 | 24 | 59 | 46 | AGACAGTGGCACTGTGACCATAAT |
| 3739 | 23 | 58 | 48 | AGACAGTGGCACTGTGACCATAA |
| 3739 | 24 | 59 | 46 | AGACAGTGGCACTGTGACCATAAT |
| 3739 | 23 | 58 | 48 | AGACAGTGGCACTGTGACCATAA |
| 3739 | 23 | 58 | 48 | AGACAGTGGCACTGTGACCATAA |
| 3739 | 23 | 58 | 48 | AGACAGTGGCACTGTGACCATAA |
| 3739 | 23 | 58 | 48 | AGACAGTGGCACTGTGACCATAA |
| 3739 | 23 | 58 | 48 | AGACAGTGGCACTGTGACCATAA |
| 3739 | 23 | 58 | 48 | AGACAGTGGCACTGTGACCATAA |
| 3739 | 23 | 58 | 48 | AGACAGTGGCACTGTGACCATAA |
| 3739 | 23 | 58 | 48 | AGACAGTGGCACTGTGACCATAA |
| 3739 | 23 | 58 | 48 | AGACAGTGGCACTGTGACCATAA |
| 3739 | 23 | 58 | 48 | AGACAGTGGCACTGTGACCATAA |
| 3739 | 24 | 59 | 46 | AGACAGTGGCACTGTGACCATAAT |
| 3739 | 23 | 58 | 48 | AGACAGTGGCACTGTGACCATAA |
| 3739 | 24 | 59 | 46 | AGACAGTGGCACTGTGACCATAAT |
| 3739 | 24 | 59 | 46 | AGACAGTGGCACTGTGACCATAAT |
| 3739 | 24 | 59 | 46 | AGACAGTGGCACTGTGACCATAAT |
| 3739 | 23 | 58 | 48 | AGACAGTGGCACTGTGACCATAA |
| 3739 | 23 | 58 | 48 | AGACAGTGGCACTGTGACCATAA |

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FIG. 5E

[illegible]

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FIG. 5F

| | | | | Probe |
|-------|--------|----|-----|---------------------------|
| Start | Length | Tm | %GC | Probe |
| 1536 | 25 | 70 | 52 | CTGGGCCATTTTGAACCTCGGGAA |
| 1536 | 23 | 68 | 57 | CTGGGCCATTTTGAACCTCGGG |
| 1536 | 24 | 69 | 54 | CTGGGCCATTTTGAACCTCGGGA |
| 1548 | 25 | 70 | 48 | TGAACCTCGGGAATTGCCAAAAGCA |
| 1534 | 24 | 68 | 54 | CACTGGGCCATTTTGAACCTCGG |
| 1532 | 25 | 70 | 52 | TGCACTGGGCCATTTTGAACCTCG |
| 1535 | 24 | 68 | 54 | ACTGGGCCATTTTGAACCTCGGG |
| 1534 | 25 | 70 | 56 | CACTGGGCCATTTTGAACCTCGGG |
| 1537 | 23 | 69 | 52 | TGGGCCATTTTGAACCTCGGGA |
| 1535 | 25 | 70 | 52 | ACTGGGCCATTTTGAACCTCGGGA |
| 1537 | 25 | 69 | 48 | TGGGCCATTTTGAACCTCGGGAAT |
| 1537 | 24 | 70 | 50 | TGGGCCATTTTGAACCTCGGGAA |
| 961 | 24 | 69 | 58 | CATGTGCAAGTCGAAAGGGCCTGC |
| 963 | 23 | 70 | 57 | TGTGCAAGTCGAAAGGGCCTGCA |
| 960 | 25 | 71 | 56 | TCATGTGCAAGTCGAAAGGGCCTGC |
| 960 | 24 | 68 | 54 | TCATGTGCAAGTCGAAAGGGCCTG |
| 962 | 24 | 69 | 54 | ATGTGCAAGTCGAAAGGGCCTGCA |
| 963 | 23 | 70 | 57 | TGTGCAAGTCGAAAGGGCCTGCA |
| 960 | 24 | 68 | 54 | TCATGTGCAAGTCGAAAGGGCCTG |
| 960 | 25 | 71 | 56 | TCATGTGCAAGTCGAAAGGGCCTGC |
| 962 | 24 | 69 | 54 | ATGTGCAAGTCGAAAGGGCCTGCA |
| 961 | 24 | 69 | 58 | CATGTGCAAGTCGAAAGGGCCTGC |
| 962 | 24 | 69 | 54 | ATGTGCAAGTCGAAAGGGCCTGCA |
| 963 | 23 | 70 | 57 | TGTGCAAGTCGAAAGGGCCTGCA |
| 960 | 24 | 68 | 54 | TCATGTGCAAGTCGAAAGGGCCTG |
| 960 | 25 | 71 | 56 | TCATGTGCAAGTCGAAAGGGCCTGC |
| 961 | 24 | 69 | 58 | CATGTGCAAGTCGAAAGGGCCTGC |
| 962 | 24 | 69 | 54 | ATGTGCAAGTCGAAAGGGCCTGCA |
| 960 | 24 | 68 | 54 | TCATGTGCAAGTCGAAAGGGCCTG |
| 961 | 24 | 69 | 58 | CATGTGCAAGTCGAAAGGGCCTGC |
| 963 | 23 | 70 | 57 | TGTGCAAGTCGAAAGGGCCTGCA |
| 960 | 25 | 71 | 56 | TCATGTGCAAGTCGAAAGGGCCTGC |
| 962 | 24 | 69 | 54 | ATGTGCAAGTCGAAAGGGCCTGCA |
| 960 | 24 | 68 | 54 | TCATGTGCAAGTCGAAAGGGCCTG |
| 960 | 25 | 71 | 56 | TCATGTGCAAGTCGAAAGGGCCTGC |
| 963 | 23 | 70 | 57 | TGTGCAAGTCGAAAGGGCCTGCA |
| 961 | 24 | 69 | 58 | CATGTGCAAGTCGAAAGGGCCTGC |
| 960 | 24 | 68 | 54 | TCATGTGCAAGTCGAAAGGGCCTG |
| 962 | 24 | 69 | 54 | ATGTGCAAGTCGAAAGGGCCTGCA |
| 961 | 24 | 69 | 58 | CATGTGCAAGTCGAAAGGGCCTGC |
| 963 | 23 | 70 | 57 | TGTGCAAGTCGAAAGGGCCTGCA |
| 960 | 25 | 71 | 56 | TCATGTGCAAGTCGAAAGGGCCTGC |
| 960 | 25 | 71 | 56 | TCATGTGCAAGTCGAAAGGGCCTGC |
| 962 | 24 | 69 | 54 | ATGTGCAAGTCGAAAGGGCCTGCA |
| 960 | 24 | 68 | 54 | TCATGTGCAAGTCGAAAGGGCCTG |

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FIG. 5G

| Probe | | | | |
|-------|--------|----|-----|---------------------------|
| Start | Length | Tm | %GC | Probe |
| 981 | 24 | 69 | 58 | CATGTGCAAGTCGAAAGGGCCTGC |
| 983 | 23 | 70 | 57 | TGTGCAAGTCGAAAGGGCCTGCA |
| 3849 | 24 | 70 | 58 | TAACCGCAGAAGGGTCATGCACCG |
| 3852 | 21 | 69 | 67 | CCGCAGAAGGGTCATGCACCG |
| 3850 | 23 | 70 | 61 | AACCGCAGAAGGGTCATGCACCG |
| 3848 | 25 | 69 | 56 | ATAACCGCAGAAGGGTCATGCACCG |
| 3855 | 23 | 68 | 61 | CAGAAGGGTCATGCACCGGCTGT |
| 3853 | 21 | 69 | 67 | CGCAGAAGGGTCATGOACCGG |
| 3851 | 22 | 69 | 64 | ACCGCAGAAGGGTCATGCACCG |
| 3850 | 23 | 70 | 61 | AACCGCAGAAGGGTCATGCACCG |
| 3852 | 21 | 69 | 67 | CCGCAGAAGGGTCATGCACCG |
| 3848 | 25 | 69 | 56 | ATAACCGCAGAAGGGTCATGCACCG |
| 3851 | 22 | 69 | 64 | ACCGCAGAAGGGTCATGCACCG |
| 3849 | 24 | 70 | 58 | TAACCGCAGAAGGGTCATGCACCG |
| 3853 | 21 | 69 | 67 | CGCAGAAGGGTCATGCACCGG |
| 3855 | 23 | 68 | 61 | CAGAAGGGTCATGCACCGGCTGT |
| 3855 | 23 | 68 | 61 | CAGAAGGGTCATGCACCGGCTGT |
| 3852 | 21 | 69 | 67 | CCGCAGAAGGGTCATGCACCG |
| 3849 | 24 | 70 | 58 | TAACCGCAGAAGGGTCATGCACCG |
| 3850 | 23 | 70 | 61 | AACCGCAGAAGGGTCATGCACCG |
| 3853 | 21 | 69 | 67 | CGCAGAAGGGTCATGCACCGG |
| 3848 | 25 | 69 | 56 | ATAACCGCAGAAGGGTCATGCACCG |
| 3851 | 22 | 69 | 64 | ACCGCAGAAGGGTCATGCACCG |
| 3853 | 21 | 69 | 67 | CGCAGAAGGGTCATGCACCGG |
| 3855 | 23 | 68 | 61 | CAGAAGGGTCATGCACCGGCTGT |
| 3848 | 25 | 69 | 56 | ATAACCGCAGAAGGGTCATGCACCG |
| 3849 | 24 | 70 | 58 | TAACCGCAGAAGGGTCATGCACCG |
| 3852 | 21 | 69 | 67 | CCGCAGAAGGGTCATGCACCG |
| 3850 | 23 | 70 | 61 | AACCGCAGAAGGGTCATGCACCG |
| 3851 | 22 | 69 | 64 | ACCGCAGAAGGGTCATGCACCG |
| 3852 | 21 | 69 | 67 | CCGCAGAAGGGTCATGCACCG |
| 3850 | 23 | 70 | 61 | AACCGCAGAAGGGTCATGCACCG |
| 3848 | 25 | 69 | 56 | ATAACCGCAGAAGGGTCATGCACCG |
| 3851 | 22 | 69 | 64 | ACCGCAGAAGGGTCATGCACCG |
| 3849 | 24 | 70 | 58 | TAACCGCAGAAGGGTCATGCACCG |
| 3855 | 23 | 68 | 61 | CAGAAGGGTCATGCACCGGCTGT |
| 3853 | 21 | 69 | 67 | CGCAGAAGGGTCATGCACCGG |
| 3850 | 23 | 70 | 61 | AACCGCAGAAGGGTCATGCACCG |
| 3855 | 23 | 68 | 61 | CAGAAGGGTCATGCACCGGCTGT |
| 3849 | 24 | 70 | 58 | TAACCGCAGAAGGGTCATGCACCG |
| 3848 | 25 | 69 | 56 | ATAACCGCAGAAGGGTCATGCACCG |
| 3853 | 21 | 69 | 67 | CGCAGAAGGGTCATGCACCGG |
| 3851 | 22 | 69 | 64 | ACCGCAGAAGGGTCATGCACCG |
| 3852 | 21 | 69 | 67 | CCGCAGAAGGGTCATGCACCG |
| 3849 | 24 | 70 | 58 | TAACCGCAGAAGGGTCATGCACCG |

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FIG. 5H

| Probe | | | | |
|-------|--------|----|-----|----------------------------|
| Start | Length | Tm | %GC | Probe |
| 3850 | 23 | 70 | 61 | AACCGCAG AAGGGTCATGCACCG |
| 3851 | 22 | 69 | 64 | ACCGCAGA AAGGGTCATGCACCG |
| 3848 | 25 | 69 | 56 | ATAACCGC AGAAGGGTCATGCACCG |
| 3852 | 21 | 69 | 67 | CCGCAGAA GGGTCATGCACCG |
| 3853 | 21 | 69 | 67 | CGCAGAAG GGTTCATGCACCGG |
| 3855 | 23 | 68 | 61 | CAGAAGGG TCATGCACCGGCTGT |
| 3853 | 21 | 69 | 67 | CGCAGAAG GGTTCATGCACCGG |
| 3855 | 23 | 68 | 61 | CAGAAGGG TCATGCACCGGCTGT |
| 3848 | 25 | 69 | 56 | ATAACCGC AGAAGGGTCATGCACCG |
| 3849 | 24 | 70 | 58 | TAACCGCA GAAGGGTCATGCACCG |
| 3852 | 21 | 69 | 67 | CCGCAGAA GGGTCATGCACCG |
| 3850 | 23 | 70 | 61 | AACCGCAG AAGGGTCATGCACCG |
| 3851 | 22 | 69 | 64 | ACCGCAGA AAGGGTCATGCACCG |
| 3853 | 21 | 69 | 67 | CGCAGAAG GGTTCATGCACCGG |
| 3855 | 23 | 68 | 61 | CAGAAGGG TCATGCACCGGCTGT |
| 3851 | 22 | 69 | 64 | ACCGCAGA AAGGGTCATGCACCG |
| 3848 | 25 | 69 | 56 | ATAACCGC AGAAGGGTCATGCACCG |
| 3850 | 23 | 70 | 61 | AACCGCAG AAGGGTCATGCACCG |
| 3852 | 21 | 69 | 67 | CCGCAGAA GGGTCATGCACCG |
| 3849 | 24 | 70 | 58 | TAACCGCA GAAGGGTCATGCACCG |
| 3850 | 23 | 70 | 61 | AACCGCAG AAGGGTCATGCACCG |
| 3853 | 21 | 69 | 67 | CGCAGAAG GGTTCATGCACCGG |
| 3848 | 25 | 69 | 56 | ATAACCGC AGAAGGGTCATGCACCG |
| 3849 | 24 | 70 | 58 | TAACCGCA GAAGGGTCATGCACCG |
| 3852 | 21 | 69 | 67 | CCGCAGAA GGGTCATGCACCG |
| 3851 | 22 | 69 | 64 | ACCGCAGA AAGGGTCATGCACCG |
| 3855 | 23 | 68 | 61 | CAGAAGGG TCATGCACCGGCTGT |
| 3851 | 22 | 69 | 64 | ACCGCAGA AAGGGTCATGCACCG |
| 3853 | 21 | 69 | 67 | CGCAGAAG GGTTCATGCACCGG |
| 3849 | 24 | 70 | 58 | TAACCGCA GAAGGGTCATGCACCG |
| 3852 | 21 | 69 | 67 | CCGCAGAA GGGTCATGCACCG |
| 3848 | 25 | 69 | 56 | ATAACCGC AGAAGGGTCATGCACCG |
| 3850 | 23 | 70 | 61 | AACCGCAG AAGGGTCATGCACCG |
| 3855 | 23 | 68 | 61 | CAGAAGGG TCATGCACCGGCTGT |
| 3853 | 21 | 69 | 67 | CGCAGAAG GGTTCATGCACCGG |
| 3852 | 21 | 69 | 67 | CCGCAGAA GGGTCATGCACCG |
| 3848 | 25 | 69 | 56 | ATAACCGC AGAAGGGTCATGCACCG |
| 3849 | 24 | 70 | 58 | TAACCGCA GAAGGGTCATGCACCG |
| 3855 | 23 | 68 | 61 | CAGAAGGG TCATGCACCGGCTGT |
| 3851 | 22 | 69 | 64 | ACCGCAGA AAGGGTCATGCACCG |
| 3850 | 23 | 70 | 61 | AACCGCAG AAGGGTCATGCACCG |
| 3851 | 22 | 69 | 64 | ACCGCAGA AAGGGTCATGCACCG |
| 3855 | 23 | 68 | 61 | CAGAAGGG TCATGCACCGGCTGT |
| 3849 | 24 | 70 | 58 | TAACCGCA GAAGGGTCATGCACCG |
| 3850 | 23 | 70 | 61 | AACCGCAG AAGGGTCATGCACCG |

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FIG. 5I

| Probe | | | | |
|-------|--------|----|-----|---------------------------|
| Start | Length | Tm | %GC | Probe |
| 3848 | 25 | 69 | 56 | ATAACCGCAGAAGGGTCATGCACCG |
| 3853 | 21 | 69 | 67 | CGCAGAAGGGTCATGCACCGG |
| 3852 | 21 | 69 | 67 | CCGCAGAAGGGTCATGCACCG |
| 3849 | 24 | 70 | 58 | TAACCGCAGAAGGGTCATGCACCG |
| 3850 | 23 | 70 | 61 | AACCGCAGAAGGGTCATGCACCG |
| 3851 | 22 | 69 | 64 | ACCGCAGAAGGGTCATGCACCG |
| 3848 | 25 | 69 | 56 | ATAACCGCAGAAGGGTCATGCACCG |
| 3855 | 23 | 68 | 61 | CAGAAGGGTCATGCACCGGCTGT |
| 3852 | 21 | 69 | 67 | CCGCAGAAGGGTCATGCACCGG |
| 3853 | 21 | 69 | 67 | CGCAGAAGGGTCATGCACCGG |
| 3850 | 23 | 70 | 61 | AACCGCAGAAGGGTCATGCACCG |
| 3851 | 22 | 69 | 64 | ACCGCAGAAGGGTCATGCACCG |
| 3852 | 21 | 69 | 67 | CCGCAGAAGGGTCATGCACCG |
| 3848 | 25 | 69 | 56 | ATAACCGCAGAAGGGTCATGCACCG |
| 3855 | 23 | 68 | 61 | CAGAAGGGTCATGCACCGGCTGT |
| 3849 | 24 | 70 | 58 | TAACCGCAGAAGGGTCATGCACCG |
| 3853 | 21 | 69 | 67 | CGCAGAAGGGTCATGCACCGG |
| 3848 | 25 | 69 | 56 | ATAACCGCAGAAGGGTCATGCACCG |
| 3855 | 23 | 68 | 61 | CAGAAGGGTCATGCACCGGCTGT |
| 3850 | 23 | 70 | 61 | AACCGCAGAAGGGTCATGCACCG |
| 3851 | 22 | 69 | 64 | ACCGCAGAAGGGTCATGCACCG |
| 3849 | 24 | 70 | 58 | TAACCGCAGAAGGGTCATGCACCG |
| 3848 | 25 | 69 | 56 | ATAACCGCAGAAGGGTCATGCACCG |
| 3849 | 24 | 70 | 58 | TAACCGCAGAAGGGTCATGCACCG |
| 3852 | 21 | 69 | 67 | CCGCAGAAGGGTCATGCACCGG |
| 3853 | 21 | 69 | 67 | CGCAGAAGGGTCATGCACCGG |
| 3853 | 21 | 69 | 67 | CGCAGAAGGGTCATGCACCGG |
| 3852 | 21 | 69 | 67 | CCGCAGAAGGGTCATGCACCG |
| 3851 | 22 | 69 | 64 | ACCGCAGAAGGGTCATGCACCG |
| 3855 | 23 | 68 | 61 | CAGAAGGGTCATGCACCGGCTGT |
| 3855 | 23 | 68 | 61 | CAGAAGGGTCATGCACCGGCTGT |
| 3853 | 21 | 69 | 67 | CGCAGAAGGGTCATGCACCGG |
| 3850 | 23 | 70 | 61 | AACCGCAGAAGGGTCATGCACCG |
| 3852 | 21 | 69 | 67 | CCGCAGAAGGGTCATGCACCG |
| 3850 | 23 | 70 | 61 | AACCGCAGAAGGGTCATGCACCG |
| 3851 | 22 | 69 | 64 | ACCGCAGAAGGGTCATGCACCG |
| 3849 | 24 | 70 | 58 | TAACCGCAGAAGGGTCATGCACCG |
| 3848 | 25 | 69 | 56 | ATAACCGCAGAAGGGTCATGCACCG |
| 3855 | 23 | 68 | 61 | CAGAAGGGTCATGCACCGGCTGT |
| 3855 | 23 | 68 | 61 | CAGAAGGGTCATGCACCGGCTGT |
| 3850 | 23 | 70 | 61 | AACCGCAGAAGGGTCATGCACCG |
| 3849 | 24 | 70 | 58 | TAACCGCAGAAGGGTCATGCACCG |
| 3851 | 22 | 69 | 64 | ACCGCAGAAGGGTCATGCACCG |
| 3848 | 25 | 69 | 56 | ATAACCGCAGAAGGGTCATGCACCG |
| 3851 | 22 | 69 | 64 | ACCGCAGAAGGGTCATGCACCG |

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FIG. 5J

| Probe | | | | |
|-------|--------|-------|-----|---------------------------|
| Start | Length | Tm... | %GC | Probe |
| 3852 | 21 | 69 | 67 | CCGCAGAAGGGTCATGCACCG |
| 3852 | 21 | 69 | 67 | CCGCAGAAGGGTCATGCACCG |
| 3849 | 24 | 70 | 58 | TAACCGCAGAAGGGTCATGCACCG |
| 3850 | 23 | 70 | 61 | AACCGCAGAAGGGTCATGCACCG |
| 3849 | 24 | 70 | 58 | TAACCGCAGAAGGGTCATGCACCG |
| 3848 | 25 | 69 | 56 | ATAACCGCAGAAGGGTCATGCACCG |
| 3853 | 21 | 69 | 67 | CGCAGAAGGGTCATGCACCGG |
| 3855 | 23 | 68 | 61 | CAGAAGGGTCATGCACCGGCTGT |
| 3853 | 21 | 69 | 67 | CGCAGAAGGGTCATGCACCGG |
| 3853 | 21 | 69 | 67 | CGCAGAAGGGTCATGCACCGG |
| 3848 | 25 | 69 | 56 | ATAACCGCAGAAGGGTCATGCACCG |
| 3852 | 21 | 69 | 67 | CCGCAGAAGGGTCATGCACCG |
| 3851 | 22 | 69 | 64 | ACCGCAGAAGGGTCATGCACCG |
| 3850 | 23 | 70 | 61 | AACCGCAGAAGGGTCATGCACCG |
| 3855 | 23 | 68 | 61 | CAGAAGGGTCATGCACCGGCTGT |
| 3849 | 24 | 70 | 58 | TAACCGCAGAAGGGTCATGCACCG |
| 3850 | 23 | 70 | 61 | AACCGCAGAAGGGTCATGCACCG |
| 3852 | 21 | 69 | 67 | CCGCAGAAGGGTCATGCACCG |
| 3851 | 22 | 69 | 64 | ACCGCAGAAGGGTCATGCACCG |
| 3853 | 21 | 69 | 67 | CGCAGAAGGGTCATGCACCGG |

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FIG. 5K

| Reverse Primer | | | | | Amplicon | | | | |
|----------------|--------|----|-----|---------------------------|----------|----|-----|----|---------|
| Start | Length | Tm | %GC | Primer | Length | Tm | %GC | Ta | Penalty |
| 1820 | 25 | 58 | 40 | AGTCCCTTTAACTGAGTTGCAATGT | 151 | 77 | 44 | 57 | 11.0 |
| 1820 | 25 | 58 | 40 | AGTCCCTTTAACTGAGTTGCAATGT | 151 | 77 | 44 | 57 | 11.0 |
| 1820 | 25 | 58 | 40 | AGTCCCTTTAACTGAGTTGCAATGT | 151 | 77 | 44 | 57 | 11.0 |
| 1820 | 25 | 58 | 40 | AGTCCCTTTAACTGAGTTGCAATGT | 151 | 77 | 44 | 57 | 11.0 |
| 1820 | 25 | 58 | 40 | AGTCCCTTTAACTGAGTTGCAATGT | 151 | 77 | 44 | 57 | 11.0 |
| 1820 | 25 | 58 | 40 | AGTCCCTTTAACTGAGTTGCAATGT | 151 | 77 | 44 | 57 | 11.0 |
| 1820 | 25 | 58 | 40 | AGTCCCTTTAACTGAGTTGCAATGT | 151 | 77 | 44 | 57 | 11.0 |
| 1820 | 25 | 58 | 40 | AGTCCCTTTAACTGAGTTGCAATGT | 151 | 77 | 44 | 57 | 11.0 |
| 1820 | 25 | 58 | 40 | AGTCCCTTTAACTGAGTTGCAATGT | 151 | 77 | 44 | 57 | 11.0 |
| 1820 | 25 | 58 | 40 | AGTCCCTTTAACTGAGTTGCAATGT | 151 | 77 | 44 | 57 | 11.0 |
| 1820 | 25 | 58 | 40 | AGTCCCTTTAACTGAGTTGCAATGT | 151 | 77 | 44 | 57 | 11.0 |
| 1026 | 25 | 58 | 44 | AAGGTTAAGACCACTACCGCAGTAA | 158 | 78 | 44 | 57 | 43.0 |
| 1026 | 25 | 58 | 44 | AAGGTTAAGACCACTACCGCAGTAA | 158 | 78 | 44 | 57 | 43.0 |
| 1026 | 25 | 58 | 44 | AAGGTTAAGACCACTACCGCAGTAA | 158 | 78 | 44 | 57 | 43.0 |
| 1026 | 25 | 58 | 44 | AAGGTTAAGACCACTACCGCAGTAA | 158 | 78 | 44 | 57 | 43.0 |
| 1026 | 25 | 58 | 44 | AAGGTTAAGACCACTACCGCAGTAA | 158 | 78 | 44 | 57 | 43.0 |
| 1026 | 25 | 58 | 44 | AAGGTTAAGACCACTACCGCAGTAA | 158 | 78 | 44 | 57 | 45.0 |
| 1026 | 25 | 58 | 44 | AAGGTTAAGACCACTACCGCAGTAA | 158 | 78 | 44 | 57 | 45.0 |
| 1026 | 25 | 58 | 44 | AAGGTTAAGACCACTACCGCAGTAA | 158 | 78 | 44 | 57 | 45.0 |
| 1026 | 25 | 58 | 44 | AAGGTTAAGACCACTACCGCAGTAA | 158 | 78 | 44 | 57 | 45.0 |
| 1026 | 25 | 58 | 44 | AAGGTTAAGACCACTACCGCAGTAA | 158 | 78 | 44 | 57 | 45.0 |
| 1026 | 25 | 58 | 44 | AAGGTTAAGACCACTACCGCAGTAA | 159 | 78 | 45 | 57 | 49.0 |
| 1026 | 25 | 58 | 44 | AAGGTTAAGACCACTACCGCAGTAA | 159 | 78 | 45 | 57 | 49.0 |
| 1026 | 25 | 58 | 44 | AAGGTTAAGACCACTACCGCAGTAA | 159 | 78 | 45 | 57 | 49.0 |
| 1026 | 25 | 58 | 44 | AAGGTTAAGACCACTACCGCAGTAA | 159 | 78 | 45 | 57 | 49.0 |
| 1026 | 25 | 58 | 44 | AAGGTTAAGACCACTACCGCAGTAA | 159 | 78 | 45 | 57 | 49.0 |
| 1026 | 25 | 58 | 44 | AAGGTTAAGACCACTACCGCAGTAA | 159 | 78 | 45 | 57 | 50.0 |
| 1026 | 25 | 58 | 44 | AAGGTTAAGACCACTACCGCAGTAA | 159 | 78 | 45 | 57 | 50.0 |
| 1026 | 25 | 58 | 44 | AAGGTTAAGACCACTACCGCAGTAA | 159 | 78 | 45 | 57 | 50.0 |
| 1026 | 25 | 58 | 44 | AAGGTTAAGACCACTACCGCAGTAA | 159 | 78 | 45 | 57 | 50.0 |
| 1026 | 25 | 58 | 44 | AAGGTTAAGACCACTACCGCAGTAA | 160 | 78 | 44 | 57 | 54.0 |
| 1026 | 25 | 58 | 44 | AAGGTTAAGACCACTACCGCAGTAA | 160 | 78 | 44 | 57 | 54.0 |
| 1026 | 25 | 58 | 44 | AAGGTTAAGACCACTACCGCAGTAA | 160 | 78 | 44 | 57 | 54.0 |
| 1026 | 25 | 58 | 44 | AAGGTTAAGACCACTACCGCAGTAA | 160 | 78 | 44 | 57 | 54.0 |
| 1026 | 25 | 58 | 44 | AAGGTTAAGACCACTACCGCAGTAA | 160 | 78 | 44 | 57 | 55.0 |
| 1026 | 25 | 58 | 44 | AAGGTTAAGACCACTACCGCAGTAA | 160 | 78 | 44 | 57 | 55.0 |
| 1026 | 25 | 58 | 44 | AAGGTTAAGACCACTACCGCAGTAA | 160 | 78 | 44 | 57 | 55.0 |
| 1026 | 25 | 58 | 44 | AAGGTTAAGACCACTACCGCAGTAA | 160 | 78 | 44 | 57 | 55.0 |
| 1026 | 25 | 58 | 44 | AAGGTTAAGACCACTACCGCAGTAA | 160 | 78 | 44 | 57 | 55.0 |
| 1026 | 25 | 58 | 44 | AAGGTTAAGACCACTACCGCAGTAA | 163 | 78 | 45 | 57 | 70.0 |
| 1026 | 25 | 58 | 44 | AAGGTTAAGACCACTACCGCAGTAA | 163 | 78 | 45 | 57 | 70.0 |
| 1026 | 25 | 58 | 44 | AAGGTTAAGACCACTACCGCAGTAA | 163 | 78 | 45 | 57 | 70.0 |

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FIG. 5L

| Reverse Primer | | | | Amplicon | | | | | | |
|----------------|--------|----|-----|----------------------------|--------|----|-----|----|---------|--|
| Start | Length | Tm | %GC | Primer | Length | Tm | %GC | Ta | Penalty | |
| 1026 | 25 | 58 | 44 | AAGGTTAAGACCAAGTACCGCAGTAA | 163 | 78 | 45 | 57 | 70.0 | |
| 1026 | 25 | 58 | 44 | AAGGTTAAGACCAAGTACCGCAGTAA | 163 | 78 | 45 | 57 | 70.0 | |
| 3921 | 22 | 59 | 41 | GTGTGCAACGTTAATTCGCAAT | 183 | 75 | 38 | 55 | 168.0 | |
| 3921 | 22 | 59 | 41 | GTGTGCAACGTTAATTCGCAAT | 183 | 75 | 38 | 55 | 168.0 | |
| 3921 | 22 | 59 | 41 | GTGTGCAACGTTAATTCGCAAT | 183 | 75 | 38 | 55 | 168.0 | |
| 3921 | 22 | 59 | 41 | GTGTGCAACGTTAATTCGCAAT | 183 | 75 | 38 | 55 | 168.0 | |
| 3921 | 22 | 59 | 41 | GTGTGCAACGTTAATTCGCAAT | 183 | 75 | 38 | 55 | 168.0 | |
| 3921 | 22 | 59 | 41 | GTGTGCAACGTTAATTCGCAAT | 183 | 75 | 38 | 55 | 168.0 | |
| 3921 | 22 | 59 | 41 | GTGTGCAACGTTAATTCGCAAT | 183 | 75 | 38 | 55 | 168.0 | |
| 3921 | 22 | 59 | 41 | GTGTGCAACGTTAATTCGCAAT | 183 | 75 | 38 | 55 | 168.0 | |
| 3921 | 22 | 59 | 41 | GTGTGCAACGTTAATTCGCAAT | 183 | 75 | 38 | 55 | 167.0 | |
| 3921 | 22 | 59 | 41 | GTGTGCAACGTTAATTCGCAAT | 183 | 75 | 38 | 55 | 167.0 | |
| 3921 | 22 | 59 | 41 | GTGTGCAACGTTAATTCGCAAT | 183 | 75 | 38 | 55 | 167.0 | |
| 3921 | 22 | 59 | 41 | GTGTGCAACGTTAATTCGCAAT | 183 | 75 | 38 | 55 | 167.0 | |
| 3921 | 22 | 59 | 41 | GTGTGCAACGTTAATTCGCAAT | 183 | 75 | 38 | 55 | 167.0 | |
| 3921 | 22 | 59 | 41 | GTGTGCAACGTTAATTCGCAAT | 183 | 75 | 38 | 55 | 167.0 | |
| 3921 | 22 | 59 | 41 | GTGTGCAACGTTAATTCGCAAT | 184 | 75 | 38 | 55 | 171.0 | |
| 3921 | 22 | 59 | 41 | GTGTGCAACGTTAATTCGCAAT | 184 | 75 | 38 | 55 | 171.0 | |
| 3921 | 22 | 59 | 41 | GTGTGCAACGTTAATTCGCAAT | 184 | 75 | 38 | 55 | 171.0 | |
| 3921 | 22 | 59 | 41 | GTGTGCAACGTTAATTCGCAAT | 184 | 75 | 38 | 55 | 171.0 | |
| 3921 | 22 | 59 | 41 | GTGTGCAACGTTAATTCGCAAT | 184 | 75 | 38 | 55 | 171.0 | |
| 3921 | 22 | 59 | 41 | GTGTGCAACGTTAATTCGCAAT | 184 | 75 | 38 | 55 | 171.0 | |
| 3921 | 22 | 59 | 41 | GTGTGCAACGTTAATTCGCAAT | 184 | 75 | 38 | 55 | 171.0 | |
| 3921 | 22 | 59 | 41 | GTGTGCAACGTTAATTCGCAAT | 184 | 75 | 38 | 55 | 172.0 | |
| 3921 | 22 | 59 | 41 | GTGTGCAACGTTAATTCGCAAT | 184 | 75 | 38 | 55 | 172.0 | |
| 3921 | 22 | 59 | 41 | GTGTGCAACGTTAATTCGCAAT | 184 | 75 | 38 | 55 | 172.0 | |
| 3921 | 22 | 59 | 41 | GTGTGCAACGTTAATTCGCAAT | 184 | 75 | 38 | 55 | 172.0 | |
| 3921 | 22 | 59 | 41 | GTGTGCAACGTTAATTCGCAAT | 184 | 75 | 38 | 55 | 172.0 | |
| 3921 | 22 | 59 | 41 | GTGTGCAACGTTAATTCGCAAT | 184 | 75 | 38 | 55 | 172.0 | |
| 3921 | 22 | 59 | 41 | GTGTGCAACGTTAATTCGCAAT | 184 | 75 | 38 | 55 | 172.0 | |
| 3921 | 22 | 59 | 41 | GTGTGCAACGTTAATTCGCAAT | 184 | 75 | 38 | 55 | 172.0 | |
| 3921 | 22 | 59 | 41 | GTGTGCAACGTTAATTCGCAAT | 184 | 75 | 38 | 55 | 173.0 | |
| 3921 | 22 | 59 | 41 | GTGTGCAACGTTAATTCGCAAT | 184 | 75 | 38 | 55 | 173.0 | |
| 3921 | 22 | 59 | 41 | GTGTGCAACGTTAATTCGCAAT | 184 | 75 | 38 | 55 | 173.0 | |
| 3921 | 22 | 59 | 41 | GTGTGCAACGTTAATTCGCAAT | 184 | 75 | 38 | 55 | 173.0 | |
| 3921 | 22 | 59 | 41 | GTGTGCAACGTTAATTCGCAAT | 184 | 75 | 38 | 55 | 173.0 | |
| 3921 | 22 | 59 | 41 | GTGTGCAACGTTAATTCGCAAT | 184 | 75 | 38 | 55 | 173.0 | |
| 3921 | 22 | 59 | 41 | GTGTGCAACGTTAATTCGCAAT | 184 | 75 | 38 | 55 | 173.0 | |
| 3921 | 22 | 59 | 41 | GTGTGCAACGTTAATTCGCAAT | 184 | 75 | 38 | 55 | 173.0 | |
| 3921 | 22 | 59 | 41 | GTGTGCAACGTTAATTCGCAAT | 185 | 75 | 38 | 55 | 177.0 | |
| 3921 | 22 | 59 | 41 | GTGTGCAACGTTAATTCGCAAT | 185 | 75 | 38 | 55 | 177.0 | |
| 3921 | 22 | 59 | 41 | GTGTGCAACGTTAATTCGCAAT | 185 | 75 | 38 | 55 | 177.0 | |
| 3921 | 22 | 59 | 41 | GTGTGCAACGTTAATTCGCAAT | 185 | 75 | 38 | 55 | 177.0 | |
| 3921 | 22 | 59 | 41 | GTGTGCAACGTTAATTCGCAAT | 185 | 75 | 38 | 55 | 177.0 | |
| 3921 | 22 | 59 | 41 | GTGTGCAACGTTAATTCGCAAT | 185 | 75 | 38 | 55 | 177.0 | |
| 3921 | 22 | 59 | 41 | GTGTGCAACGTTAATTCGCAAT | 186 | 75 | 38 | 55 | 183.0 | |

FIG. 5M

[illegible]

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FIG. 5N

[illegible]

FIG. 50

[illegible]

FIG. 6B

[illegible]

FIG. 6C

[illegible]

FIG. 6E

[illegible]

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FIG. 6F

| Probe | | | | |
|-------|--------|----|-----|---------------------------|
| Start | Length | Tm | %GC | Probe |
| 474 | 25 | 71 | 60 | TGGTGTAGGATGGGACAGTGGGCCA |
| 474 | 25 | 71 | 60 | TGGTGTAGGATGGGACAGTGGGCCA |
| 474 | 25 | 71 | 60 | TGGTGTAGGATGGGACAGTGGGCCA |
| 474 | 25 | 71 | 60 | TGGTGTAGGATGGGACAGTGGGCCA |
| 584 | 25 | 69 | 52 | TCAAGCAAGGCATGATGGACCCTCA |
| 585 | 25 | 69 | 52 | CAAGCAAGGCATGATGGACCCTCAA |
| 105 | 25 | 69 | 48 | TGTCGCATCAACAGGTGCAAATGGA |
| 474 | 25 | 71 | 60 | TGGTGTAGGATGGGACAGTGGGCCA |
| 474 | 25 | 71 | 60 | TGGTGTAGGATGGGACAGTGGGCCA |
| 474 | 25 | 71 | 60 | TGGTGTAGGATGGGACAGTGGGCCA |
| 474 | 25 | 71 | 60 | TGGTGTAGGATGGGACAGTGGGCCA |
| 474 | 25 | 71 | 60 | TGGTGTAGGATGGGACAGTGGGCCA |
| 474 | 25 | 71 | 60 | TGGTGTAGGATGGGACAGTGGGCCA |
| 474 | 25 | 71 | 60 | TGGTGTAGGATGGGACAGTGGGCCA |
| 585 | 25 | 69 | 52 | CAAGCAAGGCATGATGGACCCTCAA |
| 584 | 25 | 69 | 52 | TCAAGCAAGGCATGATGGACCCTCA |
| 585 | 25 | 69 | 52 | CAAGCAAGGCATGATGGACCCTCAA |
| 584 | 25 | 69 | 52 | TCAAGCAAGGCATGATGGACCCTCA |
| 105 | 25 | 69 | 48 | TGTCGCATCAACAGGTGCAAATGGA |
| 105 | 25 | 69 | 48 | TGTCGCATCAACAGGTGCAAATGGA |
| 105 | 25 | 69 | 48 | TGTCGCATCAACAGGTGCAAATGGA |
| 215 | 23 | 72 | 61 | ATGCCGCAAAGGCCAAGGCTGCT |
| 215 | 21 | 69 | 62 | ATGCCGCAAAGGCCAAGGCTG |
| 218 | 22 | 69 | 64 | CCGCAAAGGCCAAGGCTGCTCT |
| 218 | 24 | 71 | 63 | CCGCAAAGGCCAAGGCTGCTCTCT |
| 213 | 21 | 69 | 62 | CAATGCCGCAAAGGCCAAGGC |
| 212 | 22 | 71 | 59 | TCAATGCCGCAAAGGCCAAGGC |
| 213 | 23 | 72 | 61 | CAATGCCGCAAAGGCCAAGGCTG |
| 224 | 22 | 70 | 68 | AGGCCAAGGCTGCTCTCTCGCG |
| 223 | 24 | 71 | 63 | AAGGCCAAGGCTGCTCTCTCGCGT |
| 227 | 24 | 68 | 63 | CCAAGGCTGCTCTCTCGCGTAAGC |
| 219 | 23 | 69 | 61 | CGCAAAGGCCAAGGCTGCTCTCT |
| 221 | 24 | 70 | 63 | CAAAGGCCAAGGCTGCTCTCTCGC |
| 224 | 24 | 70 | 63 | AGGCCAAGGCTGCTCTCTCGCGTA |
| 222 | 25 | 71 | 60 | AAAGGCCAAGGCTGCTCTCTCGCGT |
| 211 | 23 | 71 | 61 | CTCAATGCCGCAAAGGCCAAGGC |
| 206 | 23 | 69 | 57 | TCTTCCTCAATGCCGCAAAGGCC |
| 207 | 23 | 70 | 57 | CTTCCTCAATGCCGCAAAGGCCA |
| 206 | 24 | 71 | 54 | TCTTCCTCAATGCCGCAAAGGCCA |
| 205 | 25 | 72 | 52 | TTCTTCCTCAATGCCGCAAAGGCCA |
| 203 | 25 | 69 | 52 | TCTTCCTCAATGCCGCAAAGGCC |
| 204 | 25 | 70 | 56 | CTTCTTCCTCAATGCCGCAAAGGCC |
| 205 | 24 | 70 | 54 | TTCTTCCTCAATGCCGCAAAGGCC |
| 209 | 23 | 70 | 57 | TCCTCAATGCCGCAAAGGCCAAG |
| 210 | 23 | 71 | 61 | CCTCAATGCCGCAAAGGCCAAGG |

FIG. 6G

| Probe | | | | |
|-------|--------|----|-----|-----------------------------|
| Start | Length | Tm | %GC | Probe |
| 209 | 21 | 69 | 57 | TCCTCAATGCCGCAAAGGCCA |
| 208 | 23 | 70 | 52 | TTCCTCAATGCCGCAAAGGCCAA |
| 207 | 25 | 71 | 56 | CTTCCTCAATGCCGCAAAGGCCAAG |
| 213 | 22 | 70 | 59 | CAATGCCGCAAAGGCCAAGGCT |
| 218 | 21 | 69 | 67 | CCGCAAAGGCCAAGGCTGCTC |
| 212 | 23 | 71 | 57 | TCAATGCCGCAAAGGCCAAGGCT |
| 206 | 25 | 72 | 52 | TCTTCCTCAATGCCGCAAAGGCCAA |
| 215 | 22 | 72 | 64 | ATGCCGCAAAGGCCAAGGCTGC |
| 214 | 22 | 70 | 59 | AATGCCGCAAAGGCCAAGGCTG |
| 216 | 20 | 69 | 65 | TGCCGCAAAGGCCAAGGCTG |
| 211 | 24 | 71 | 58 | CTCAATGCCGCAAAGGCCAAGGCT |
| 208 | 24 | 70 | 54 | TTCCTCAATGCCGCAAAGGCCAAG |
| 208 | 22 | 69 | 55 | TTCCTCAATGCCGCAAAGGCCA |
| 207 | 24 | 70 | 54 | CTTCCTCAATGCCGCAAAGGCCAA |
| 209 | 22 | 69 | 55 | TCCTCAATGCCGCAAAGGCCAA |
| 210 | 22 | 68 | 59 | CCTCAATGCCGCAAAGGCCAAG |
| 211 | 22 | 68 | 59 | CTCAATGCCGCAAAGGCCAAGG |
| 224 | 23 | 70 | 65 | AGGCCAAGGCTGCTCTCTCGCGT |
| 216 | 21 | 72 | 67 | TGCCGCAAAGGCCAAGGCTGC |
| 227 | 25 | 70 | 64 | CCAAGGCTGCTCTCTCGCGTAAGCC |
| 228 | 25 | 70 | 60 | CAAGGCTGCTCTCTCGCGTAAGCCA |
| 229 | 24 | 68 | 58 | AAGGCTGCTCTCTCTCGCGTAAGCCA |
| 224 | 25 | 70 | 60 | AGGCCAAGGCTGCTCTCTCGCGTAA |
| 229 | 25 | 68 | 60 | AAGGCTGCTCTCTCTCGCGTAAGCCAG |
| 223 | 25 | 70 | 60 | AAGGCCAAGGCTGCTCTCTCGCGTA |
| 218 | 23 | 71 | 65 | CCGCAAAGGCCAAGGCTGCTCTC |
| 219 | 24 | 70 | 63 | CGCAAAGGCCAAGGCTGCTCTCTC |
| 219 | 22 | 68 | 64 | CGCAAAGGCCAAGGCTGCTCTC |
| 223 | 23 | 70 | 65 | AAGGCCAAGGCTGCTCTCTCGCG |
| 228 | 24 | 68 | 63 | CAAGGCTGCTCTCTCGCGTAAGCC |
| 222 | 24 | 71 | 63 | AAAGGCCAAGGCTGCTCTCTCGCG |
| 219 | 22 | 68 | 64 | CGCAAAGGCCAAGGCTGCTCTC |
| 216 | 20 | 69 | 65 | TGCCGCAAAGGCCAAGGCTG |
| 218 | 21 | 69 | 67 | CCGCAAAGGCCAAGGCTGCTC |
| 215 | 22 | 72 | 64 | ATGCCGCAAAGGCCAAGGCTGC |
| 218 | 23 | 71 | 65 | CCGCAAAGGCCAAGGCTGCTCTC |
| 214 | 22 | 70 | 59 | AATGCCGCAAAGGCCAAGGCTG |
| 213 | 22 | 70 | 59 | CAATGCCGCAAAGGCCAAGGCT |
| 223 | 25 | 70 | 60 | AAGGCCAAGGCTGCTCTCTCGCGTA |
| 224 | 23 | 70 | 65 | AGGCCAAGGCTGCTCTCTCGCGT |
| 224 | 25 | 70 | 60 | AGGCCAAGGCTGCTCTCTCGCGTAA |
| 219 | 24 | 70 | 63 | CGCAAAGGCCAAGGCTGCTCTCTC |
| 222 | 24 | 71 | 63 | AAAGGCCAAGGCTGCTCTCTCGCG |
| 223 | 23 | 70 | 65 | AAGGCCAAGGCTGCTCTCTCGCG |
| 206 | 25 | 72 | 52 | TCTTCCTCAATGCCGCAAAGGCCAA |

FIG. 6H

| Probe | | | | |
|-------|--------|----|-----|-----------------------------|
| Start | Length | Tm | %GC | Probe |
| 210 | 22 | 68 | 59 | CCTCAATGCCGCAAAGGCCAAG |
| 205 | 25 | 72 | 52 | TTCTTCCTCAATGCCGCAAAGGCCA |
| 204 | 25 | 70 | 56 | CTTCTTCCTCAATGCCGCAAAGGCC |
| 206 | 23 | 69 | 57 | TCTTCCTCAATGCCGCAAAGGCC |
| 206 | 24 | 71 | 54 | TCTTCCTCAATGCCGCAAAGGCCA |
| 205 | 24 | 70 | 54 | TTCTTCCTCAATGCCGCAAAGGCC |
| 211 | 24 | 71 | 58 | CTCAATGCCGCAAAGGCCAAGGCT |
| 209 | 22 | 69 | 55 | TCCTCAATGCCGCAAAGGCCAA |
| 207 | 24 | 70 | 54 | CTTCCTCAATGCCGCAAAGGCCAA |
| 203 | 25 | 69 | 52 | TCTTCCTTCCTCAATGCCGCAAAGGC |
| 208 | 24 | 70 | 54 | TTCTTCCTCAATGCCGCAAAGGCCAAG |
| 211 | 22 | 68 | 59 | CTCAATGCCGCAAAGGCCAAGG |
| 208 | 22 | 69 | 55 | TTCTTCCTCAATGCCGCAAAGGCCA |
| 213 | 21 | 69 | 62 | CAATGCCGCAAAGGCCAAGGC |
| 213 | 23 | 72 | 61 | CAATGCCGCAAAGGCCAAGGCTG |
| 211 | 23 | 71 | 61 | CTCAATGCCGCAAAGGCCAAGGC |
| 212 | 22 | 71 | 59 | TCAATGCCGCAAAGGCCAAGGC |
| 212 | 23 | 71 | 57 | TCAATGCCGCAAAGGCCAAGGCT |
| 216 | 21 | 72 | 67 | TGCCGCAAAGGCCAAGGCTGC |
| 216 | 23 | 72 | 61 | ATGCCGCAAAGGCCAAGGCTGCT |
| 215 | 21 | 69 | 62 | ATGCCGCAAAGGCCAAGGCTG |
| 208 | 23 | 70 | 52 | TTCTTCCTCAATGCCGCAAAGGCCAA |
| 207 | 25 | 71 | 56 | CTTCCTCAATGCCGCAAAGGCCAAG |
| 210 | 23 | 71 | 61 | CCTCAATGCCGCAAAGGCCAAGG |
| 209 | 21 | 69 | 57 | TCCTCAATGCCGCAAAGGCCA |
| 207 | 23 | 70 | 57 | CTTCCTCAATGCCGCAAAGGCCA |
| 209 | 23 | 70 | 57 | TCCTCAATGCCGCAAAGGCCAAG |
| 228 | 24 | 68 | 63 | CAAGGCTGCTCTCTCGCGTAAGCC |
| 227 | 25 | 70 | 64 | CCAAGGCTGCTCTCTCGCGTAAGCC |
| 227 | 24 | 68 | 63 | CCAAGGCTGCTCTCTCGCGTAAGC |
| 224 | 24 | 70 | 63 | AGGCCAAGGCTGCTCTCTCGCGTA |
| 229 | 24 | 68 | 58 | AAGGCTGCTCTCTCGCGTAAGCCA |
| 218 | 22 | 69 | 64 | CCGCAAAGGCCAAGGCTGCTCT |
| 229 | 25 | 68 | 60 | AAGGCTGCTCTCTCTCGCGTAAGCCAG |
| 228 | 25 | 70 | 60 | CAAGGCTGCTCTCTCTCGCGTAAGCCA |
| 218 | 24 | 71 | 63 | CCGCAAAGGCCAAGGCTGCTCTCT |
| 221 | 24 | 70 | 63 | CAAAGGCCAAGGCTGCTCTCTCGC |
| 219 | 23 | 69 | 61 | CGCAAAGGCCAAGGCTGCTCTCT |
| 224 | 22 | 70 | 68 | AGGCCAAGGCTGCTCTCTCGCG |
| 223 | 24 | 71 | 63 | AAGGCCAAGGCTGCTCTCTCGCGT |
| 222 | 25 | 71 | 60 | AAAGGCCAAGGCTGCTCTCTCGCGT |
| 474 | 25 | 71 | 60 | TGGTGTAGGATGGGACAGTGGGCCA |
| 474 | 25 | 71 | 60 | TGGTGTAGGATGGGACAGTGGGCCA |
| 474 | 25 | 71 | 60 | TGGTGTAGGATGGGACAGTGGGCCA |
| 474 | 25 | 71 | 60 | TGGTGTAGGATGGGACAGTGGGCCA |

FIG. 6I

| Probe | | | | |
|-------|--------|----|-----|----------------------------|
| Start | Length | Tm | %GC | Probe |
| 474 | 25 | 71 | 60 | TGGTGTAGGATGGGACAGTGGGCCA |
| 474 | 25 | 71 | 60 | TGGTGTAGGATGGGACAGTGGGCCA |
| 474 | 25 | 71 | 60 | TGGTGTAGGATGGGACAGTGGGCCA |
| 474 | 25 | 71 | 60 | TGGTGTAGGATGGGACAGTGGGCCA |
| 474 | 25 | 71 | 60 | TGGTGTAGGATGGGACAGTGGGCCA |
| 584 | 25 | 69 | 52 | TCAAGCAAGGCATGATGGACCCTCA |
| 585 | 25 | 69 | 52 | CAAGCAAGGCATGATGGACCCTCAA |
| 584 | 25 | 69 | 52 | TCAAGCAAGGCATGATGGACCCTCA |
| 585 | 25 | 69 | 52 | CAAGCAAGGCATGATGGACCCTCAA |
| 584 | 25 | 69 | 52 | TCAAGCAAGGCATGATGGACCCTCA |
| 585 | 25 | 69 | 52 | CAAGCAAGGCATGATGGACCCTCAA |
| 222 | 25 | 71 | 60 | AAAGGCCAAGGCTGCTCTCTCGCGT |
| 218 | 24 | 71 | 63 | CCGCAAAGGCCAAGGCTGCTCTCT |
| 218 | 23 | 71 | 65 | CCGCAAAGGCCAAGGCTGCTCTC |
| 224 | 25 | 70 | 60 | AGGCCAAGGCTGCTCTCTCGCGTAA |
| 224 | 22 | 70 | 68 | AGGCCAAGGCTGCTCTCTCGCG |
| 224 | 23 | 70 | 65 | AGGCCAAGGCTGCTCTCTCGCGT |
| 224 | 24 | 70 | 63 | AGGCCAAGGCTGCTCTCTCGCGTA |
| 216 | 20 | 69 | 65 | TGCCGCAAAGGCCAAGGCTG |
| 215 | 23 | 72 | 61 | ATGCCGCAAAGGCCAAGGCTGCT |
| 218 | 21 | 69 | 67 | CCGCAAAGGCCAAGGCTGCTC |
| 216 | 21 | 72 | 67 | TGCCGCAAAGGCCAAGGCTGC |
| 219 | 22 | 68 | 64 | CGCAAAGGCCAAGGCTGCTCTC |
| 219 | 23 | 69 | 61 | CGCAAAGGCCAAGGCTGCTCTCT |
| 229 | 25 | 68 | 60 | AAGGCTGCTCTCTCGCGTAAGCCAG |
| 228 | 25 | 70 | 60 | CAAGGCTGCTCTCTCGCGTAAGCCA |
| 227 | 24 | 68 | 63 | CCAAGGCTGCTCTCTCGCGTAAGC |
| 229 | 24 | 68 | 58 | AAGGCTGCTCTCTCGCGTAAGCCA |
| 228 | 24 | 68 | 63 | CAAGGCTGCTCTCTCGCGTAAGCC |
| 223 | 25 | 70 | 60 | AAGGCCAAGGCTGCTCTCTCGCGTA |
| 227 | 25 | 70 | 64 | CCAAGGCTGCTCTCTCGCGTAAGCC |
| 223 | 24 | 71 | 63 | AAGGCCAAGGCTGCTCTCTCGCGT |
| 223 | 23 | 70 | 65 | AAGGCCAAGGCTGCTCTCTCGCG |
| 218 | 22 | 69 | 64 | CCGCAAAGGCCAAGGCTGCTCT |
| 221 | 24 | 70 | 63 | CAAAGGCCAAGGCTGCTCTCTCGC |
| 219 | 24 | 70 | 63 | CGCAAAGGCCAAGGCTGCTCTCTC |
| 222 | 24 | 71 | 63 | AAAGGCCAAGGCTGCTCTCTCGCG |
| 207 | 25 | 71 | 56 | CTTCCTCAATGCCGCAAAGGCCAAG |
| 208 | 24 | 70 | 54 | TTCCTCAATGCCGCAAAGGCCAAG |
| 208 | 23 | 70 | 52 | TTCCTCAATGCCGCAAAGGCCAA |
| 211 | 22 | 68 | 59 | CTCAATGCCGCAAAGGCCAAGG |
| 206 | 25 | 72 | 52 | TCTTCCTCAATGCCGCAAAGGCCAA |
| 207 | 23 | 70 | 57 | CTTCCTCAATGCCGCAAAGGCCA |
| 207 | 24 | 70 | 54 | CTTCCTCAATGCCGCAAAGGCCAA |
| 203 | 25 | 69 | 52 | TCTTCCTTCCTCAATGCCGCAAAGGC |

FIG. 6J

| Probe | | | | |
|-------|--------|----|-----|---------------------------|
| Start | Length | Tm | %GC | Probe |
| 206 | 24 | 71 | 54 | TCTTCCTCAATGCCGCAAAGGCCA |
| 205 | 24 | 70 | 54 | TTCTTCCTCAATGCCGCAAAGGCC |
| 204 | 25 | 70 | 56 | CTTCTTCCTCAATGCCGCAAAGGCC |
| 208 | 22 | 69 | 55 | TTCCTCAATGCCGCAAAGGCCA |
| 206 | 23 | 69 | 57 | TCTTCCTCAATGCCGCAAAGGCC |
| 205 | 25 | 72 | 52 | TTCTTCCTCAATGCCGCAAAGGCCA |
| 214 | 22 | 70 | 59 | AATGCCGCAAAGGCCAAGGCTG |
| 209 | 23 | 70 | 57 | TCCTCAATGCCGCAAAGGCCAAG |
| 210 | 23 | 71 | 61 | CCTCAATGCCGCAAAGGCCAAGG |
| 211 | 23 | 71 | 61 | CTCAATGCCGCAAAGGCCAAGGC |
| 209 | 22 | 69 | 55 | TCCTCAATGCCGCAAAGGCCAA |
| 209 | 21 | 69 | 57 | TCCTCAATGCCGCAAAGGCCA |
| 213 | 21 | 69 | 62 | CAATGCCGCAAAGGCCAAGGC |
| 213 | 23 | 72 | 61 | CAATGCCGCAAAGGCCAAGGCTG |
| 211 | 24 | 71 | 58 | CTCAATGCCGCAAAGGCCAAGGCT |
| 215 | 21 | 69 | 62 | ATGCCGCAAAGGCCAAGGCTG |
| 210 | 22 | 68 | 59 | CCTCAATGCCGCAAAGGCCAAG |
| 212 | 23 | 71 | 57 | TCAATGCCGCAAAGGCCAAGGCT |
| 213 | 22 | 70 | 59 | CAATGCCGCAAAGGCCAAGGCT |
| 212 | 22 | 71 | 59 | TCAATGCCGCAAAGGCCAAGGC |

FIG. 6K

[illegible]

[illegible]

FIG. 6M

[illegible]

FIG. 6N

[illegible]

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FIG. 7A

| Forward Primer | | | | |
|----------------|--------|----|-----|---------------------------|
| Start | Length | Tm | %GC | Primer |
| 6062 | 21 | 59 | 43 | AAAGTCGGGCTTGACGAATTT |
| 6062 | 21 | 59 | 43 | AAAGTCGGGCTTGACGAATTT |
| 6062 | 21 | 59 | 43 | AAAGTCGGGCTTGACGAATTT |
| 6061 | 22 | 59 | 41 | TAAAGTCGGGCTTGACGAATTT |
| 6061 | 22 | 59 | 41 | TAAAGTCGGGCTTGACGAATTT |
| 6061 | 22 | 59 | 41 | TAAAGTCGGGCTTGACGAATTT |
| 6062 | 21 | 59 | 43 | AAAGTCGGGCTTGACGAATTT |
| 6062 | 21 | 59 | 43 | AAAGTCGGGCTTGACGAATTT |
| 6060 | 22 | 59 | 41 | TTAAAGTCGGGCTTGACGAATT |
| 6060 | 22 | 59 | 41 | TTAAAGTCGGGCTTGACGAATT |
| 6060 | 23 | 60 | 39 | TTAAAGTCGGGCTTGACGAATTT |
| 6061 | 22 | 59 | 41 | TAAAGTCGGGCTTGACGAATTT |
| 6060 | 22 | 59 | 41 | TTAAAGTCGGGCTTGACGAATT |
| 6060 | 23 | 60 | 39 | TTAAAGTCGGGCTTGACGAATTT |
| 6061 | 22 | 59 | 41 | TAAAGTCGGGCTTGACGAATTT |
| 6060 | 23 | 60 | 39 | TTAAAGTCGGGCTTGACGAATTT |
| 6062 | 21 | 59 | 43 | AAAGTCGGGCTTGACGAATTT |
| 6059 | 23 | 59 | 39 | ATTAAAGTCGGGCTTGACGAATT |
| 6060 | 22 | 59 | 41 | TTAAAGTCGGGCTTGACGAATT |
| 6059 | 24 | 60 | 38 | ATTAAAGTCGGGCTTGACGAATTT |
| 6059 | 23 | 59 | 39 | ATTAAAGTCGGGCTTGACGAATT |
| 6060 | 23 | 60 | 39 | TTAAAGTCGGGCTTGACGAATTT |
| 6060 | 22 | 59 | 41 | TTAAAGTCGGGCTTGACGAATT |
| 6061 | 22 | 59 | 41 | TAAAGTCGGGCTTGACGAATTT |
| 6059 | 24 | 60 | 38 | ATTAAAGTCGGGCTTGACGAATTT |
| 6059 | 23 | 59 | 39 | ATTAAAGTCGGGCTTGACGAATT |
| 6060 | 23 | 60 | 39 | TTAAAGTCGGGCTTGACGAATTT |
| 6059 | 24 | 60 | 38 | ATTAAAGTCGGGCTTGACGAATTT |
| 6058 | 22 | 59 | 45 | GATTAAAGTCGGGCTTGACGAA |
| 6058 | 22 | 59 | 45 | GATTAAAGTCGGGCTTGACGAA |
| 6058 | 23 | 59 | 43 | GATTAAAGTCGGGCTTGACGAAT |
| 6058 | 24 | 61 | 42 | GATTAAAGTCGGGCTTGACGAATT |
| 6058 | 22 | 59 | 45 | GATTAAAGTCGGGCTTGACGAA |
| 6058 | 23 | 59 | 43 | GATTAAAGTCGGGCTTGACGAAT |
| 6059 | 23 | 59 | 39 | ATTAAAGTCGGGCTTGACGAATT |
| 6060 | 22 | 59 | 41 | TTAAAGTCGGGCTTGACGAATT |
| 6058 | 24 | 61 | 42 | GATTAAAGTCGGGCTTGACGAATT |
| 6058 | 23 | 59 | 43 | GATTAAAGTCGGGCTTGACGAAT |
| 6059 | 24 | 60 | 38 | ATTAAAGTCGGGCTTGACGAATTT |
| 6059 | 23 | 59 | 39 | ATTAAAGTCGGGCTTGACGAATT |
| 6060 | 23 | 60 | 39 | TTAAAGTCGGGCTTGACGAATTT |
| 6058 | 24 | 61 | 42 | GATTAAAGTCGGGCTTGACGAATT |
| 6059 | 24 | 60 | 38 | ATTAAAGTCGGGCTTGACGAATTT |
| 6058 | 25 | 62 | 40 | GATTAAAGTCGGGCTTGACGAATTT |
| 6058 | 22 | 59 | 45 | GATTAAAGTCGGGCTTGACGAA |

FIG. 7B

| Forward Primer | | | | |
|----------------|--------|----|-----|---------------------------|
| Start | Length | Tm | %GC | Primer |
| 6058 | 22 | 59 | 45 | GATTAAAGTCGGGCTTGACGAA |
| 6058 | 23 | 59 | 43 | GATTAAAGTCGGGCTTGACGAAT |
| 6058 | 23 | 59 | 43 | GATTAAAGTCGGGCTTGACGAAT |
| 6058 | 24 | 61 | 42 | GATTAAAGTCGGGCTTGACGAATT |
| 6059 | 23 | 59 | 39 | ATTAAAGTCGGGCTTGACGAATT |
| 6058 | 24 | 61 | 42 | GATTAAAGTCGGGCTTGACGAATT |
| 6058 | 25 | 62 | 40 | GATTAAAGTCGGGCTTGACGAATTT |
| 6059 | 24 | 60 | 38 | ATTAAAGTCGGGCTTGACGAATTT |
| 6058 | 25 | 62 | 40 | GATTAAAGTCGGGCTTGACGAATTT |
| 6058 | 22 | 59 | 45 | GATTAAAGTCGGGCTTGACGAA |
| 6058 | 23 | 59 | 43 | GATTAAAGTCGGGCTTGACGAAT |
| 6058 | 24 | 61 | 42 | GATTAAAGTCGGGCTTGACGAATT |
| 6058 | 25 | 62 | 40 | GATTAAAGTCGGGCTTGACGAATTT |
| 6054 | 22 | 59 | 45 | CAAGGATTAAAGTCGGGCTTGA |
| 6054 | 22 | 59 | 45 | CAAGGATTAAAGTCGGGCTTGA |
| 6054 | 23 | 60 | 48 | CAAGGATTAAAGTCGGGCTTGAC |
| 6054 | 22 | 59 | 45 | CAAGGATTAAAGTCGGGCTTGA |
| 6054 | 23 | 60 | 48 | CAAGGATTAAAGTCGGGCTTGAC |
| 6054 | 23 | 60 | 48 | CAAGGATTAAAGTCGGGCTTGAC |
| 6053 | 23 | 61 | 43 | TCAAGGATTAAAGTCGGGCTTGA |
| 6054 | 22 | 59 | 45 | CAAGGATTAAAGTCGGGCTTGA |
| 6053 | 23 | 61 | 43 | TCAAGGATTAAAGTCGGGCTTGA |
| 6053 | 24 | 61 | 46 | TCAAGGATTAAAGTCGGGCTTGAC |
| 6054 | 23 | 60 | 48 | CAAGGATTAAAGTCGGGCTTGAC |
| 6054 | 22 | 59 | 45 | CAAGGATTAAAGTCGGGCTTGA |
| 6053 | 23 | 61 | 43 | TCAAGGATTAAAGTCGGGCTTGA |
| 6053 | 24 | 61 | 46 | TCAAGGATTAAAGTCGGGCTTGAC |
| 6054 | 23 | 60 | 48 | CAAGGATTAAAGTCGGGCTTGAC |
| 6053 | 24 | 61 | 46 | TCAAGGATTAAAGTCGGGCTTGAC |
| 6053 | 23 | 61 | 43 | TCAAGGATTAAAGTCGGGCTTGA |
| 6054 | 22 | 59 | 45 | CAAGGATTAAAGTCGGGCTTGA |
| 6053 | 23 | 61 | 43 | TCAAGGATTAAAGTCGGGCTTGA |
| 6053 | 24 | 61 | 46 | TCAAGGATTAAAGTCGGGCTTGAC |
| 6054 | 23 | 60 | 48 | CAAGGATTAAAGTCGGGCTTGAC |
| 6052 | 24 | 62 | 42 | TTCAAGGATTAAAGTCGGGCTTGA |
| 6053 | 24 | 61 | 46 | TCAAGGATTAAAGTCGGGCTTGAC |
| 6052 | 24 | 62 | 42 | TTCAAGGATTAAAGTCGGGCTTGA |
| 6053 | 23 | 61 | 43 | TCAAGGATTAAAGTCGGGCTTGA |
| 6052 | 24 | 62 | 42 | TTCAAGGATTAAAGTCGGGCTTGA |
| 6053 | 24 | 61 | 46 | TCAAGGATTAAAGTCGGGCTTGAC |
| 6052 | 24 | 62 | 42 | TTCAAGGATTAAAGTCGGGCTTGA |

FIG. 7C

[illegible]

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FIG. 7D

[illegible]

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FIG. 7E

| Reverse Primer | | | | | Amplicon | | | | |
|----------------|--------|----|-----|---------------------------|----------|----|-----|----|---------|
| Start | Length | Tm | %GC | Primer | Length | Tm | %GC | Ta | Penalty |
| 6298 | 23 | 59 | 48 | CGGACAGAAACTCTAAGCCATCA | 235 | 74 | 35 | 54 | 427.0 |
| 6298 | 24 | 59 | 46 | CGGACAGAAACTCTAAGCCATCAT | 235 | 74 | 35 | 54 | 428.0 |
| 6298 | 25 | 61 | 44 | CGGACAGAAACTCTAAGCCATCATT | 235 | 74 | 35 | 54 | 429.0 |
| 6298 | 23 | 59 | 48 | CGGACAGAAACTCTAAGCCATCA | 236 | 74 | 35 | 54 | 431.0 |
| 6298 | 24 | 59 | 46 | CGGACAGAAACTCTAAGCCATCAT | 236 | 74 | 35 | 54 | 432.0 |
| 6298 | 25 | 61 | 44 | CGGACAGAAACTCTAAGCCATCATT | 236 | 74 | 35 | 54 | 433.0 |
| 6297 | 24 | 61 | 46 | TCGGACAGAAACTCTAAGCCATCA | 236 | 74 | 35 | 54 | 433.0 |
| 6297 | 25 | 61 | 44 | TCGGACAGAAACTCTAAGCCATCAT | 236 | 74 | 35 | 54 | 434.0 |
| 6296 | 23 | 59 | 48 | CGGACAGAAACTCTAAGCCATCA | 237 | 74 | 35 | 54 | 436.0 |
| 6296 | 24 | 59 | 46 | CGGACAGAAACTCTAAGCCATCAT | 237 | 74 | 35 | 54 | 437.0 |
| 6296 | 23 | 59 | 48 | CGGACAGAAACTCTAAGCCATCA | 237 | 74 | 35 | 54 | 437.0 |
| 6297 | 24 | 61 | 46 | TCGGACAGAAACTCTAAGCCATCA | 237 | 74 | 35 | 54 | 437.0 |
| 6298 | 25 | 61 | 44 | CGGACAGAAACTCTAAGCCATCATT | 237 | 74 | 35 | 54 | 438.0 |
| 6296 | 24 | 59 | 46 | CGGACAGAAACTCTAAGCCATCAT | 237 | 74 | 35 | 54 | 438.0 |
| 6297 | 25 | 61 | 44 | TCGGACAGAAACTCTAAGCCATCAT | 237 | 74 | 35 | 54 | 438.0 |
| 6296 | 25 | 61 | 44 | CGGACAGAAACTCTAAGCCATCATT | 237 | 74 | 35 | 55 | 439.0 |
| 6298 | 25 | 61 | 44 | ATCGGACAGAAACTCTAAGCCATCA | 237 | 74 | 35 | 54 | 439.0 |
| 6296 | 23 | 59 | 48 | CGGACAGAAACTCTAAGCCATCA | 238 | 74 | 35 | 54 | 442.0 |
| 6297 | 24 | 61 | 46 | TCGGACAGAAACTCTAAGCCATCA | 238 | 74 | 35 | 54 | 442.0 |
| 6296 | 23 | 59 | 48 | CGGACAGAAACTCTAAGCCATCA | 238 | 74 | 35 | 54 | 443.0 |
| 6296 | 24 | 59 | 46 | CGGACAGAAACTCTAAGCCATCAT | 238 | 74 | 35 | 54 | 443.0 |
| 6297 | 24 | 61 | 46 | TCGGACAGAAACTCTAAGCCATCA | 238 | 74 | 35 | 55 | 443.0 |
| 6297 | 25 | 61 | 44 | TCGGACAGAAACTCTAAGCCATCAT | 238 | 74 | 35 | 54 | 443.0 |
| 6298 | 25 | 61 | 44 | ATCGGACAGAAACTCTAAGCCATCA | 238 | 74 | 35 | 54 | 443.0 |
| 6296 | 24 | 59 | 46 | CGGACAGAAACTCTAAGCCATCAT | 238 | 74 | 35 | 54 | 444.0 |
| 6296 | 25 | 61 | 44 | CGGACAGAAACTCTAAGCCATCATT | 238 | 74 | 35 | 54 | 444.0 |
| 6297 | 25 | 61 | 44 | TCGGACAGAAACTCTAAGCCATCAT | 238 | 74 | 35 | 55 | 444.0 |
| 6296 | 25 | 61 | 44 | CGGACAGAAACTCTAAGCCATCATT | 238 | 74 | 35 | 55 | 445.0 |
| 6296 | 23 | 59 | 48 | CGGACAGAAACTCTAAGCCATCA | 239 | 74 | 35 | 54 | 446.0 |
| 6296 | 24 | 59 | 46 | CGGACAGAAACTCTAAGCCATCAT | 239 | 74 | 35 | 54 | 447.0 |
| 6296 | 23 | 59 | 48 | CGGACAGAAACTCTAAGCCATCA | 239 | 74 | 35 | 54 | 447.0 |
| 6296 | 23 | 59 | 48 | CGGACAGAAACTCTAAGCCATCA | 239 | 74 | 35 | 54 | 448.0 |
| 6296 | 25 | 61 | 44 | CGGACAGAAACTCTAAGCCATCATT | 239 | 74 | 35 | 54 | 448.0 |
| 6296 | 24 | 59 | 46 | CGGACAGAAACTCTAAGCCATCAT | 239 | 74 | 35 | 55 | 448.0 |
| 6297 | 24 | 61 | 46 | TCGGACAGAAACTCTAAGCCATCA | 239 | 74 | 35 | 54 | 448.0 |
| 6298 | 25 | 61 | 44 | ATCGGACAGAAACTCTAAGCCATCA | 239 | 74 | 35 | 54 | 448.0 |
| 6296 | 24 | 59 | 46 | CGGACAGAAACTCTAAGCCATCAT | 239 | 74 | 35 | 55 | 449.0 |
| 6296 | 25 | 61 | 44 | CGGACAGAAACTCTAAGCCATCATT | 239 | 74 | 35 | 55 | 449.0 |
| 6297 | 24 | 61 | 46 | TCGGACAGAAACTCTAAGCCATCA | 239 | 74 | 35 | 55 | 449.0 |
| 6297 | 25 | 61 | 44 | TCGGACAGAAACTCTAAGCCATCAT | 239 | 74 | 35 | 54 | 449.0 |
| 6298 | 25 | 61 | 44 | ATCGGACAGAAACTCTAAGCCATCA | 239 | 74 | 35 | 55 | 449.0 |
| 6296 | 25 | 61 | 44 | CGGACAGAAACTCTAAGCCATCATT | 239 | 74 | 35 | 55 | 450.0 |
| 6297 | 25 | 61 | 44 | TCGGACAGAAACTCTAAGCCATCAT | 239 | 74 | 35 | 55 | 450.0 |
| 6296 | 25 | 61 | 44 | CGGACAGAAACTCTAAGCCATCATT | 239 | 74 | 35 | 55 | 451.0 |
| 6297 | 24 | 61 | 46 | TCGGACAGAAACTCTAAGCCATCA | 240 | 74 | 35 | 54 | 452.0 |

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FIG. 7F

| Reverse Primer | | | | | Amplicon | | | | |
|----------------|--------|----|-----|---------------------------|----------|----|-----|----|---------|
| Start | Length | Tm | %GC | Primer | Length | Tm | %GC | Ta | Penalty |
| 6297 | 25 | 61 | 44 | TCGGACAGAAACTCTAACCCATCAT | 240 | 74 | 35 | 54 | 453.0 |
| 6297 | 24 | 61 | 46 | TCGGACAGAAACTCTAACCCATCA | 240 | 74 | 35 | 54 | 453.0 |
| 6297 | 25 | 61 | 44 | TCGGACAGAAACTCTAACCCATCAT | 240 | 74 | 35 | 54 | 454.0 |
| 6297 | 24 | 61 | 46 | TCGGACAGAAACTCTAACCCATCA | 240 | 74 | 35 | 55 | 454.0 |
| 6298 | 25 | 61 | 44 | ATCGGACAGAAACTCTAACCCATCA | 240 | 73 | 35 | 54 | 454.0 |
| 6297 | 25 | 61 | 44 | TCGGACAGAAACTCTAACCCATCAT | 240 | 74 | 35 | 55 | 455.0 |
| 6297 | 24 | 61 | 46 | TCGGACAGAAACTCTAACCCATCA | 240 | 74 | 35 | 55 | 455.0 |
| 6298 | 25 | 61 | 44 | ATCGGACAGAAACTCTAACCCATCA | 240 | 73 | 35 | 55 | 455.0 |
| 6297 | 25 | 61 | 44 | TCGGACAGAAACTCTAACCCATCAT | 240 | 74 | 35 | 55 | 456.0 |
| 6298 | 25 | 61 | 44 | ATCGGACAGAAACTCTAACCCATCA | 241 | 74 | 35 | 54 | 458.0 |
| 6298 | 25 | 61 | 44 | ATCGGACAGAAACTCTAACCCATCA | 241 | 74 | 35 | 54 | 459.0 |
| 6298 | 25 | 61 | 44 | ATCGGACAGAAACTCTAACCCATCA | 241 | 74 | 35 | 55 | 460.0 |
| 6298 | 25 | 61 | 44 | ATCGGACAGAAACTCTAACCCATCA | 241 | 74 | 35 | 55 | 461.0 |
| 6296 | 23 | 59 | 48 | CGGACAGAAACTCTAACCCATCA | 243 | 74 | 35 | 54 | 466.0 |
| 6296 | 24 | 59 | 46 | CGGACAGAAACTCTAACCCATCAT | 243 | 74 | 35 | 55 | 467.0 |
| 6296 | 23 | 59 | 48 | CGGACAGAAACTCTAACCCATCA | 243 | 74 | 35 | 54 | 467.0 |
| 6296 | 25 | 61 | 44 | CGGACAGAAACTCTAACCCATCATT | 243 | 74 | 35 | 55 | 468.0 |
| 6296 | 24 | 59 | 46 | CGGACAGAAACTCTAACCCATCAT | 243 | 74 | 35 | 55 | 468.0 |
| 6296 | 25 | 61 | 44 | CGGACAGAAACTCTAACCCATCATT | 243 | 74 | 35 | 55 | 469.0 |
| 6296 | 23 | 59 | 48 | CGGACAGAAACTCTAACCCATCA | 244 | 74 | 35 | 54 | 472.0 |
| 6297 | 24 | 61 | 46 | TCGGACAGAAACTCTAACCCATCA | 244 | 74 | 35 | 54 | 472.0 |
| 6296 | 24 | 59 | 46 | CGGACAGAAACTCTAACCCATCAT | 244 | 74 | 35 | 55 | 473.0 |
| 6296 | 23 | 59 | 48 | CGGACAGAAACTCTAACCCATCA | 244 | 74 | 35 | 54 | 473.0 |
| 6297 | 24 | 61 | 46 | TCGGACAGAAACTCTAACCCATCA | 244 | 74 | 35 | 55 | 473.0 |
| 6297 | 25 | 61 | 44 | TCGGACAGAAACTCTAACCCATCAT | 244 | 74 | 35 | 54 | 473.0 |
| 6296 | 25 | 61 | 44 | CGGACAGAAACTCTAACCCATCATT | 244 | 74 | 35 | 55 | 474.0 |
| 6296 | 24 | 59 | 46 | CGGACAGAAACTCTAACCCATCAT | 244 | 74 | 35 | 55 | 474.0 |
| 6297 | 25 | 61 | 44 | TCGGACAGAAACTCTAACCCATCAT | 244 | 74 | 35 | 55 | 474.0 |
| 6296 | 25 | 61 | 44 | CGGACAGAAACTCTAACCCATCATT | 244 | 74 | 35 | 55 | 475.0 |
| 6297 | 24 | 61 | 46 | TCGGACAGAAACTCTAACCCATCA | 245 | 74 | 35 | 55 | 478.0 |
| 6298 | 25 | 61 | 44 | ATCGGACAGAAACTCTAACCCATCA | 245 | 74 | 35 | 54 | 478.0 |
| 6297 | 25 | 61 | 44 | TCGGACAGAAACTCTAACCCATCAT | 245 | 74 | 35 | 55 | 479.0 |
| 6297 | 24 | 61 | 46 | TCGGACAGAAACTCTAACCCATCA | 245 | 74 | 35 | 55 | 479.0 |
| 6298 | 25 | 61 | 44 | ATCGGACAGAAACTCTAACCCATCA | 245 | 74 | 35 | 55 | 479.0 |
| 6296 | 25 | 61 | 44 | CGGACAGAAACTCTAACCCATCATT | 245 | 74 | 35 | 55 | 480.0 |
| 6297 | 25 | 61 | 44 | TCGGACAGAAACTCTAACCCATCAT | 245 | 74 | 35 | 55 | 480.0 |
| 6297 | 24 | 61 | 46 | TCGGACAGAAACTCTAACCCATCA | 246 | 74 | 35 | 55 | 484.0 |
| 6298 | 25 | 61 | 44 | ATCGGACAGAAACTCTAACCCATCA | 246 | 74 | 35 | 55 | 484.0 |
| 6297 | 25 | 61 | 44 | TCGGACAGAAACTCTAACCCATCAT | 246 | 74 | 35 | 55 | 485.0 |
| 6298 | 25 | 61 | 44 | ATCGGACAGAAACTCTAACCCATCA | 246 | 74 | 35 | 55 | 485.0 |
| 6298 | 25 | 61 | 44 | ATCGGACAGAAACTCTAACCCATCA | 247 | 74 | 35 | 55 | 490.0 |

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Envelope Protein Purification Flow-Chart

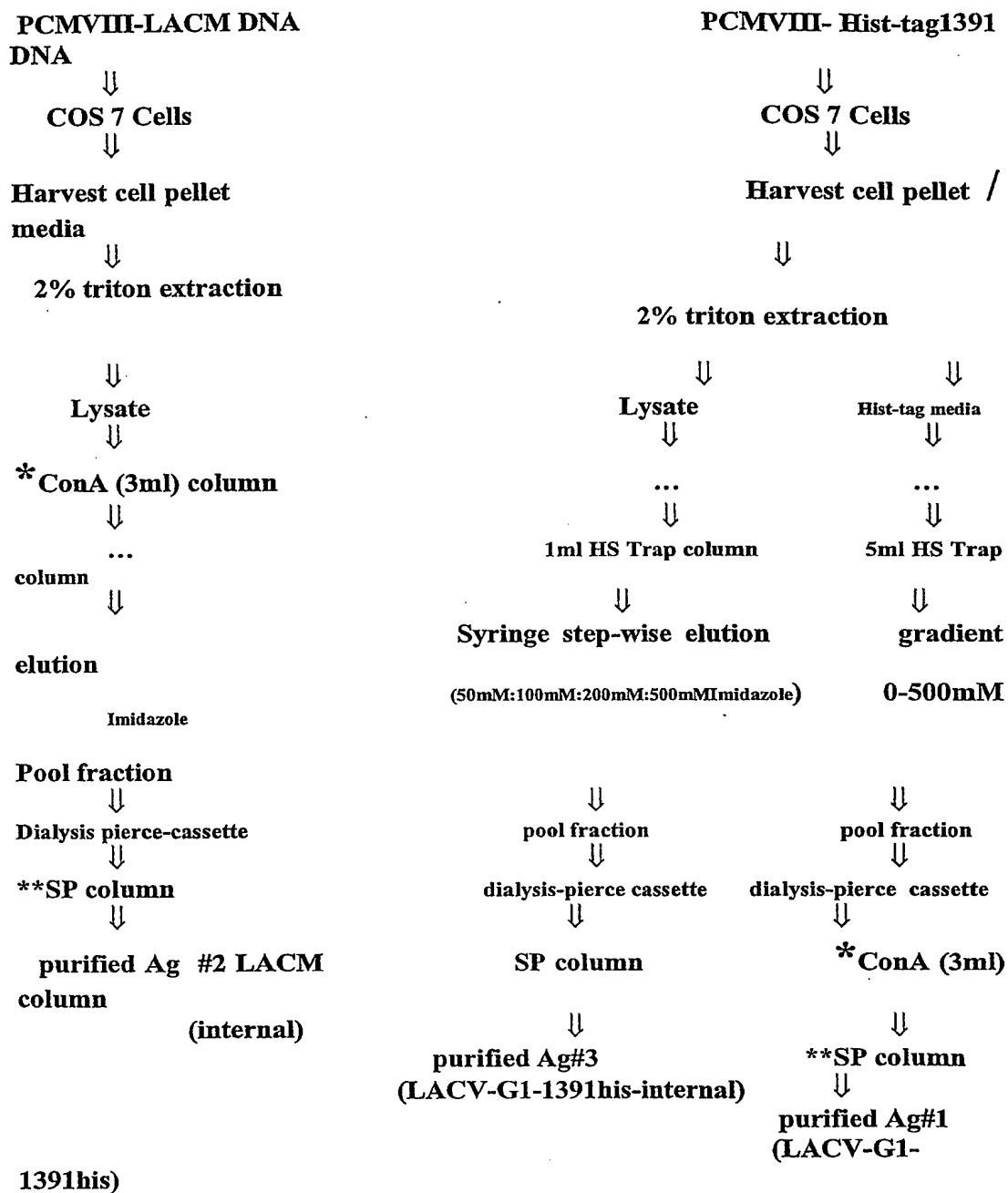


FIGURE 8

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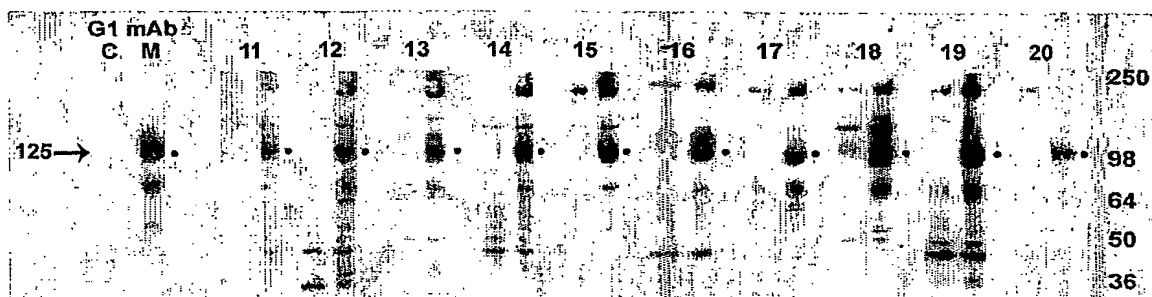


Figure 9A

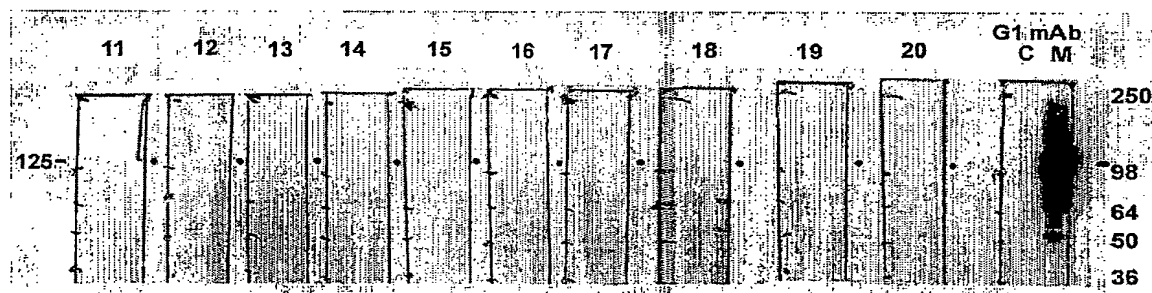


Figure 9B

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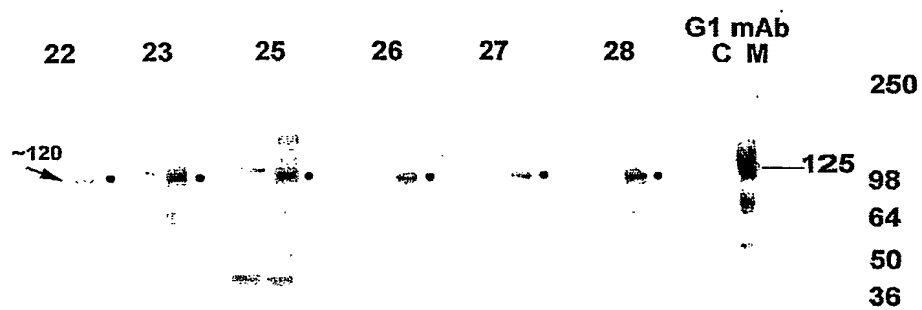


Figure 10A

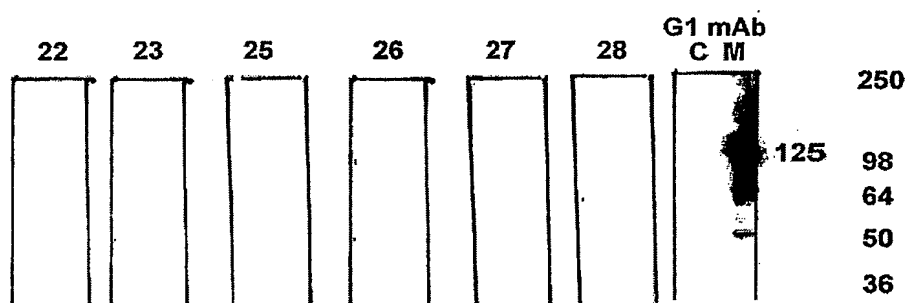


Figure 10B

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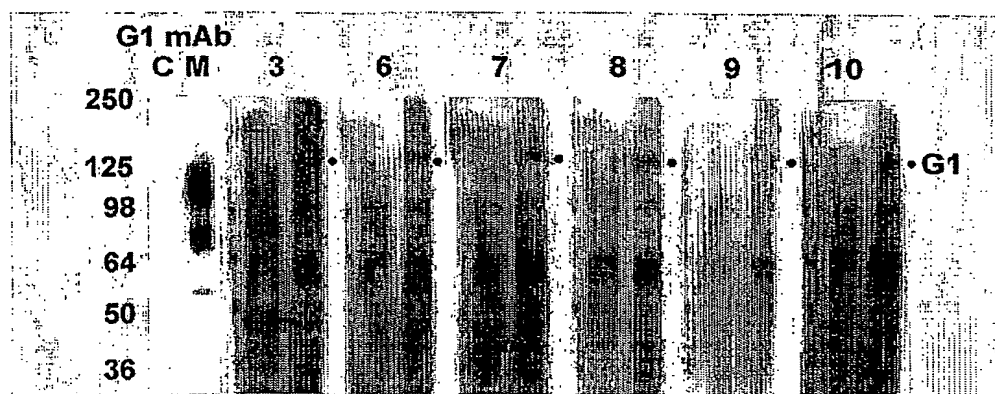


Figure 11A

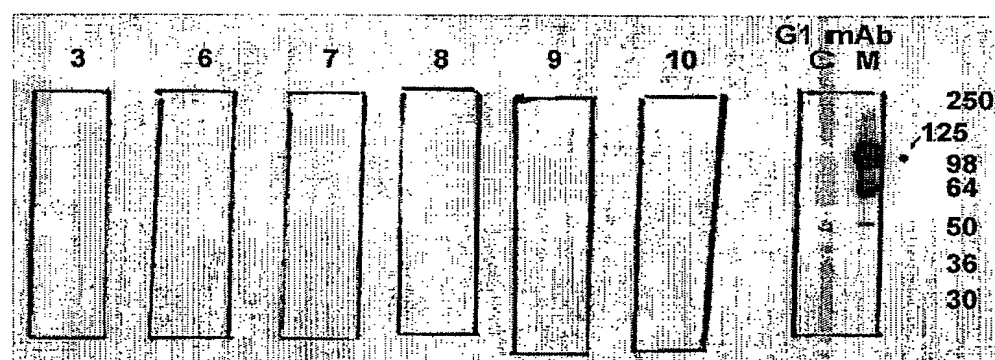


Figure 11B

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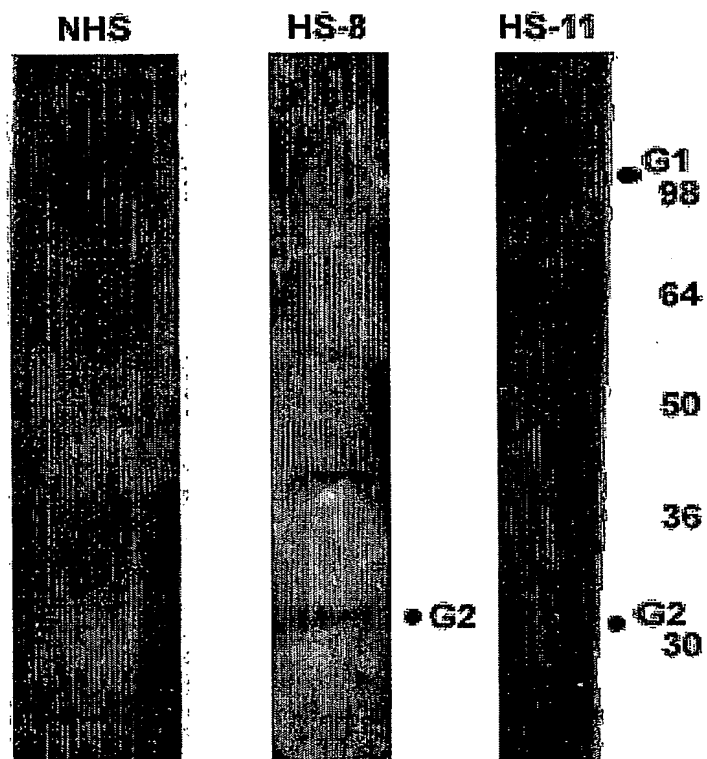


FIGURE 12A

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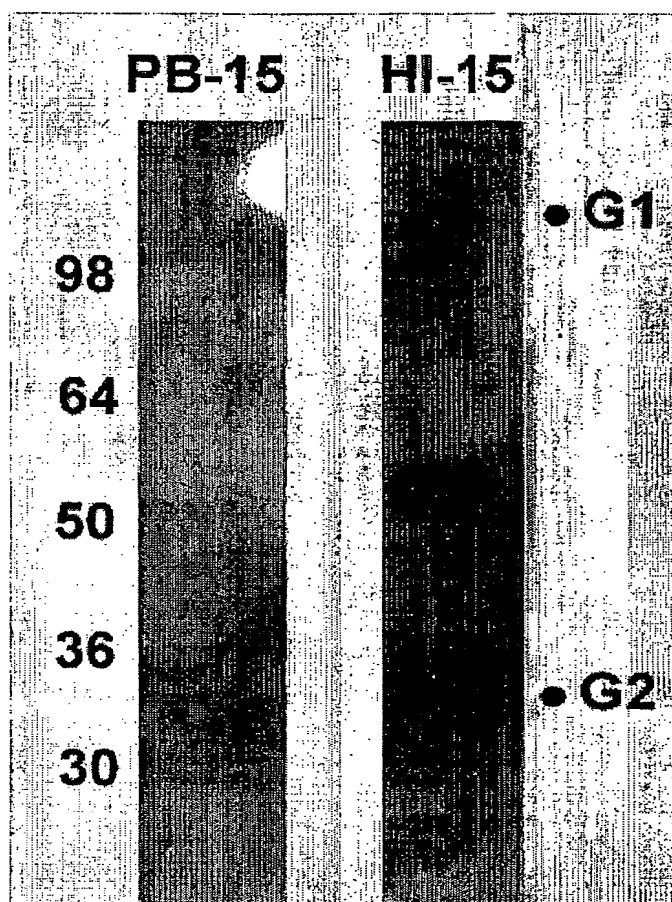


FIGURE 12B